

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTC**ATG**GCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCTATTCCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

**FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902  
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown  
><MW: -1, pI: 8.36, NX(S/T): 1  
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCGCCGCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT  
GTTCCCTCTTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGGTGCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGCCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCCTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
GGCAGTAATACGGACTCTTGTAAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

113-117



**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTGAGCCCATTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG  
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTTCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
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**FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT  
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT  
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG  
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
CTGATCAATAATGCTGGTGTTCGCGGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTTCGCCTTGCA  
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG  
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAAGGCAGTTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG  
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGTT  
AAGTATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT  
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW  
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF  
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEgyIEKSLD  
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK  
AELANPKAV

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCCGTCGCCACCACT  
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTCCTCCTTGCCTTTCTGCTTTTCTGT  
 GGA**CTCCTCTTCTACATCAACTTGGCTGACCATTGGA**AAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAA**AAACCAGCAAATCCACCCG**TCTTACCAG  
 CTCCTCAGAAGGCGGACACCGACCCCTGAGAACTTACCTGAGATTTCGTACAGAAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCTGTGGATCCCCGCCCGGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTTCAAGAAGAGCAGAAGTGCCCA**CAAGCCTCCCT**GCCACCGGCCAGGACACAGGG  
 CACACCAGTGCATCTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCTGCATGCATGGA  
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
 GAGGAAAGAAATTTGAGGAAGCCAGGAAGTGGGTGTCAAGAAGTTACACTTTGAAAAGGACG  
 TGGACGTCAACCTGTTT**GAGAGCACGATCCGCATCCT**GGGGGGGCTCCTGAGTGCCTACCAC  
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATT**CAGCTGGAGTTCCGG**  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTT**CATCAATA**CCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGT**CAGAACGCACCTGCTGCGGCACTCCGAGCC**AGTAAGCTCACCTTTG  
 TGGGGGAGCTTGCCACGGCCGCTT**CAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA**  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCAGGA  
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
 TGCATTTCAACCTTTACCC**CCAGCCGGCCGTCGGGACGTGGAGGTCAAGCCAGCAGACAGG**  
 CACAACCTGCTGCGGCCAGAGACCGTGAGAGCCTGTTCTACCTGTACCGCGT**CACAGGGGA**  
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATT**CACACGGGTCC**  
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCCCTCTGCCTATCT  
 GGACCCCTGCC**CTAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
 CTGGGTCTGTGGCATT**TTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCC**CAGGCT  
 CTGAACCTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
 GGCCGTCACTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCTC  
 CAGAAGACACGAATCATGACTACGATTGGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
 GAGGGGGGCTTCAGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGACAGCCAGGGTGCAGC  
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC  
 CTGGCCGCCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCT  
 CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

### FIGURE 10

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
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><subunit 1 of 1, 699 aa, 1 stop
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><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSTFGESYDN  
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE  
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT  
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPARTQGTPVHLNY  
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA  
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
PYSVDNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK  
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
HLLRHSEPSKLTFFVGE LAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVGTGRKYQDWG  
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD  
AYVFENTEAHPLPIWTPA

Important features of the protein:

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
GCCCCTCGGGAATCACAACTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG  
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AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGACATTC  
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
GGACCCCCCTGCCTTCCTGCTCACCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGG  
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC  
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR  
GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFPEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI  
TTGYKTRHRLHDPARWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTATACAAAGATATTAAGGC  
CCTGTTCAATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTGTAAAGATTGTTCTGTGT  
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## **FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

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GGGACCATATGCGGCCGTGACACCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACGAGCAAAAG  
GAGCATGTCCGCGCCGGGAAGGCCCGTCTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG  
GCCC GCGCCGCGCTCTCTGCCGCCCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
CTCGCCCCG CAGGCCCGGCCCGCAGC**ATGG**AGCCACCCGGACGCCGGCGGGGCCGCGCGCA  
GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGGCG  
GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC  
AGGGCGGCGGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT  
GCCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCC  
AGCTGAAGAATGGCTCATTTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAA  
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GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAATCTGGTTC  
GGCTAAACCTTTGCGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG  
TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT  
GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCTCCGCTT  
GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT  
TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG  
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC  
TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTGAGGCTGGATCTACTGGAAATTG  
GGGCTGTCATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGCGCGAGATGTGATAGAGGTGGCT  
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TTACACTGTGGAAGCAGCCAACTTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
TTGAAAAATTTTGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
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TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT  
ACTGGCTTCACGGGGATGACCTGTACCGTGTTCCAGAAAGTGGCAGCCTCTGATCGTACAGG  
ACTTTGCGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT  
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
AAGACTATTTACAGTT**TAAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
AAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT  
CTTCACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACT  
ATTGTTACATGTGAAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTGCTCCT  
GATTTTAAGACAATAAGATGTTTTCATGGGCCCCCTAAAAGTATCATGAGCCTTTGGCACTGC  
GCCTGCCAAGCCTAGTGAGGAGAAGTCAACCTGAGACCAGGTGTTTAATCAAGCAAGCTGTAT  
ATCAAAATTTTTTGGCAGAAAAACACAAATATGTATATATCTTTTTTAAAAAAGTATTTCA  
TTGAAGCAAGCAAAATGAAAGCATTTTTACTGATTTTTAAAATTTGGTGCTTTTAGATATATT  
GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCCCTAATGGAACCACATT  
TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG  
TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAATGGC  
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA  
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSLELAQVLPDTPNRTVTILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
 FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELEPSFYMT  
 SHRQVVFEGDSLPPQCMASYIDQDMQVLWYQDGRIVETDESQGFVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTL  
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMP  
 LNL TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIAS  
 NIMLA DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTG  
 FTMCT VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFK  
 TIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560

CCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAA  
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

## **FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**FIGURE 19**

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACC  
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTGCTTCTCCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
 CTATGTCCAGTTCCCTGTCCCACGGCCGTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCCGGCCCGGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCCCTGTGCGGGCTGGCCTTGCTGTC  
 TGTCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTCTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCTTTCCTCTGTTTTCTCTTCTGTCTCCCCTCCCTCCCACCTTTTTCTTTCTTCC  
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCCTTCCCTTTCCTCTTGCTGT  
 TTCCTTCTGTGTTGTTTTGTTGCCACATCCTGTTTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG  
 TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCGCTGTCGGCTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCCATGCCACAGCCCC  
 CCAAGGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT  
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAAACATATATATATATAT  
 ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG  
 CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT  
 CTGTGGTATGAAAAAG

**FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTIVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPI TFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI  
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFKV

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

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[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFShPKVHMDPNYCHPSTSLHLCS  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTTCCCT  
GGCACCCCTCCTGCTCAGTGCGACATTGTCACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACA**ATG**TTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA  
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAACTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAACTCTTTCCAA  
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAGGAAAAC  
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
CATCCTAGCCTTTTGACAAATTCTCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTTCTTACAATTTTTTGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

**FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSSNF TWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA  
MPESEENARDGIPMDDIPPLRTSV

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

**FIGURE 25**

[illegible]

**FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF  
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG  
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR  
HFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTCTGGCGGGAGCACCCAGTCCTGTACGCC  
AAGGAACTGGTCCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCTCTGTGCCCCCTGAAGGCCACGTT  
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG  
GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
GCTGATTGCTGTGGTGGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGCCCG  
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG  
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG  
GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGCAGCAGTGTCCACCCCAG  
TGTCTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTGGGGCCCCCAAGTGGTCACCTCCCC  
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGCCCTCCCTGTGG  
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA  
GCTACAGGGTAAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG  
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
GATCAGGTTGAATGAATGGAACCTCTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
TGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCCTGCTTTAGGGAGGCT  
CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCCAACCTCTGCACAGCTCT  
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA  
AAGA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLILLLLLSVLPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPPTNFLDGI VDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP  
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPGPPESPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248



**FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
 GGGAGGACAGGGAGTTCGGAAGGAGGAGGACAGAGGAGGGGCACAGAGACGCAGAGCAAGGGCG  
 GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAG**ATG**  
 AAGTTCCAGGGGGCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG  
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC  
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGGCAGCT  
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
 GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG  
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA  
 GATGCTGTCCGCGGCTCCTGGCAGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG  
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG  
 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT  
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC  
 TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTTCAGTGAGAGCCAGCAACCAGAATGAAGGT  
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC  
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG  
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG  
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGA  
 TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACC  
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTTCAGGGCTTCA  
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGA  
 GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT  
 TGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT  
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA  
 AGCTCTCGCATCCCC**TGA**CCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACT  
 CCCTCCTTAAAACACCACCCTCTCATCACTAATCTCAGCCCTTGGCCTTGAAATAAACCTTA  
 GCTGCCCCACAAA  
 AA

**FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA  
 AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGM  
 NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS  
 GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSGSSSGSGSSSGNSGGSRGDSGSESSW  
 GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL  
 GSGSDNYRGQGSWSGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDINKDQ  
 RSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCGGGCGGTGCTCACCG  
TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA  
CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGTCGAGGAGAGTGAGGGGAAGATGTGTTTCTGAACAAGC  
TGCTGCTACTTGCTGTCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTTCTTTTGGAAAGAGG  
GTCCCTCATATGCCTTTGAGGTGGACACAGTAGAGCTCCGAGCATGGCTTGGACAATGCGCCTGTGGTGACCAAG  
AGCTGCTCTACACTGCTGCCCCATACATCGGAGAGCTCCGGAACCTGCTCGCTTCTGGGTGTGAGGCAGTAGTG  
GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTTCCAGACCA  
GCCAGGGGCTGCAGGCACAGCTCGCCAGGCCTTTTTCCACAACCAGCCGCCCTCCTTGCGCCGACCGTAGAGT  
TCGTGGCAGAAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG  
CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCCCAGCTGTTGGAGATCT  
TGTGTTCCAGCTGTGCCCTCACGGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG  
GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCCGCGACCGTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC  
TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAAATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
TGAGTCGCACACTTCGAGCCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCTTGAC  
GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC  
CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG  
GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATTCTAGGCGCCCCGCACAGTACAGGCTGGAGAGAGG  
CAGGCTCGAAGCCTTCTGCACATGCTGCTTCTTGTGGAAGGAAGACTTTAGGGGCGGTTCCGCTGCAGCTG  
TCTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA  
CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCTGCCTGGGCAGCCTCCACCAGGCCAG  
TGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC  
CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC  
CTGCCCTTGGGCATTGCACCAGAACCCTGGACCCCCGCTCACGAGGAGGCCAAAGTCCCCAATGCAGACCCCTAC  
TGTTTGGGGTAGCTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGTTCTACTGCCTGGCATCCCCACACGCG  
ATCCTTAGAGTAAGGAGAGATTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTTGGAGTAGAA  
GAGGTGGTGTGTTTGTGTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAAGCCT  
CATTTGCTATCCCAGCATCTCTTAAACCTTTGTAGTCTTGGAAATTCATGACAGAGGCAAATGACTCCTGCTTAAAC  
TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCCTGAGGTGCGCG  
GACTGCTGAGGTGAGGAATTCAGACAGCCTGGCCAAATGGCAAAACCCCATCTCTACTAAAAATAAAAAA  
TTATTAGCTGGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC  
CTGGAGGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTCTAG  
AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTTCAGCCCCCT  
TGCAGGTAGTAACCTCTTGGACCTCTCCCTGACCCAGGACCACAGCACAGGGCATTTAGAGCTTTTTAGAAATAA  
CTGGTTTTCTTTAAAAAATAAAAAAAGGGCGGGCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
TTTTTTTTTTTTTTTTAAAAAAGGGCTTTTATTAATAATTCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC  
TGGGGCGTGTCTGTAGGGAAGGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG  
GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG  
AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCCTGTCTTAACCGACACCCCTGAGGTGCTCCTGAGATGCTG  
GGTCCACCCTGAGTGGCACGGGAGCAGCTGTGGCCCGTGTCTTCTCTAGGCGAGCTTCTGGGGAACATAGCTC  
GGGCCCTTCTTTGCAAGACCGAGGATGGGTGGGTGTGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGT  
GAAGAGGGCGCGGGTTTTGTTGGCTGCAGCGGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTTCCGTCTA  
ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGGACGAGCGTCAT  
GTTATTTTCACTGCTGCTGCGACGTTGGCCTGGGCACGTGATGGAATGGCCATGTCCCTCTGCTGCGTGGAC  
GTGCGCGTGGGAGTGCAGCCAGAGCGGGGCCAGAGCTGCGCTGGGGGTGAGGGAGGCGCCCGGGAGGG  
CCTCAGAGGAAGTTGGGCTCCCGCACCAAGCAGGCGGGCTCCCGCGCGCGCGCCAGCACCCTGAGG  
GGCCGCTAGACAAGTGAAGTGCAGCTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCAGCAGCGG  
TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGCGCT

**FIGURE 32**

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
 SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL  
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
 IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

**FIGURE 33**

TCCCTTGACAGGTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC  
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**  
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAAAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGAGCAGCTCCAGCCACCTGCT  
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCATTC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
 CATCTTCTGGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG  
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT  
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG  
 GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCCGCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCCGAGCAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA  
 TCACCTTCTCCCACCCCTCCTGGACCT**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCTAG  
 AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTTG  
 CCCCCCAATTTCCAGCACCAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTGTGTGGAGGTGTGGGGGCGGTGGGGAGGTCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG  
 CACCCTTCTGCCCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCTTTCCACCTCCCCTACAA  
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCCAGCCACTATCCCTTGCTGGAAGGCT  
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTC  
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT  
 CTAGCAGGGAGGTTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCCCTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTCTGCTGGGATGGCTGTGCGGAGCTGT  
 ATCACCTGGGTTCTGTCCCCGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG  
 GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC  
 TCCGGAAA

**FIGURE 34**

MSSNKEQRSADFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
 GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
 SSVFRLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELCDHVHVYGMVPPNYCSQRPRLQRMPIH  
 YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

GTTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT  
 GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG  
 GGCAAAGGTGAAAGAGTTTTCAGAACAAGCTTCCTGGAACCCATGACCCATGAAGTCTTGTGACATTTTATACCGT  
 CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGTCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC  
 GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
 AGGCTTGAGTCCACACTGGCTTGCTCCTCCTAGCAGAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG  
 GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGAACCTCCA  
 AGGATGAATGTAACCTGGCGCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC  
 CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCTGCG  
 GGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG  
 ATTGAAGTGGATGAGGGAAACACAGCAGTCAATTGCCTGCCACCTGCCTGAGAGCCACCCCAAAGCCAGGTCCGG  
 TACAGCGTCAAACAAGAGTGGCTGGAGGCCCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAAACC  
 TCCGCTTCCAGCTACGTGTGCGCCCTCCACCTGAGGTCAAGTCAAGTGGAGCTATCCAGCTGGTGCATCCCTGGGGC  
 CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCCACCCACGGGTG  
 ACCTGGGCAAGGATGGGTCCAGTGTACCCGGCTACAACAAGACGCGCTTCCTGCTGAGCAACCTCCTCATCGAC  
 ACCACGAGGAGGAGTCCAGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGACGCCCGGGGACGCGGT  
 ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTCAAGTCAAGTGGAGCTATCCAGCTGGTGCATCCCTGGGGC  
 CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCGGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC  
 CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTCAGCATGGGGCTGAGGACGAAGGC  
 GTCTACCAAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCTAGCTAGTCCAGCTGCGGACCTCCAGGCCAAGC  
 ATAACCCCAAGGCTATGGCAGGATGCTGAGTGGCTTGGCAGACCTCCTGTATCACCTCCAAACTCGGCAAC  
 CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCGAGACCCCAACGTGAGTGGGGCTGCTTCCCCGAAGTGT  
 CCAGGAGAGAAGGGGACGGGGGCTCCCGCCGAGGCTCCCATCATCCTCAGCTCGCCCCGACCTCCAAGACAGAC  
 TCATATGAAGTGGTGTGGCGGCTCGGCATGAGGCGAGTGGCCGGGCGCAATCCTTACTATGTGGTGAACAC  
 CGCAAGCAGGTACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACAGCACCGCCTGACCCTC  
 ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCGGGAGAGGGCCAGACAGCC  
 ATGGTCACCTTCCGAAGTGGAGCGGCGGCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC  
 GACCTTGGAGCCAGTCCCGAGAGCAGCAGCCAGCCAGCCAGCCGCGCTCTCCCCCAGAAGCTCCCGACAGG  
 CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCCAATC  
 CAGTCCCTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA  
 TCGCGGCTGTCCGTGGAGATCACGGGCTTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG  
 CTGGGGGAGAGCGAGCCAGCGCCCTCTCGGCCCTACGTGGTGTGCGGCTACAGCGGTGCGGTGTACGAGAGG  
 CCCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC  
 CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAACATGATAGT  
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC  
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTGAGCAACGTGATGATCTGTGAGACCAAAGCT  
 CGGAAGTCTTCTGGCCAGCCTGGTTCGACTGCCACCCCAACTCTGGCCCCACCACAGCCGCCCCCTCCTGAAACC  
 ATAGAGCGGCGGCTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGTC  
 CTGGGCTCCATCGTCTCATCATCGTCACCTTCATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT  
 ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCTCCTGCCCCGTATACTATGGTGCCATTGGGAGGACTC  
 CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCAGGGCAGCTTCAG  
 CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCAAGTCAACGATC  
 ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTTCTTATACACACTGCCCGACGACTCCACTCACCAGCTG  
 CTGCAGCCCATCAGCACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC  
 CCCGACAGTCTGTCTGGAAGCAGTGTGGGACCTCATTTCACTCAGGGCCCCCATGCTGCTTGGGCCTTGTG  
 CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGCACCCCTAGGG  
 GCCTACGTAGGACAGGAACCTGGAATGCAGTCTCCCCGGGGCCACTGGTGGTGTGCTTTTTGAAACACCACCT  
 CTCACAAT**TAGG**CAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAAAGAAGAAAA  
 AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAATAAATGTA  
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGGAAAAATAAAGAAGCTGCCA  
 CCTAACAGGAGTCAACCAGGAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCCTCTGCAGTG  
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCACGAGCA  
 TGAGGGAACAGCAAGGGGCACGCTATCACAGCTGGAGACCCACACAGATGGCTGGATCCGGTGTACGGGAA  
 ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAATAAACCTTCAGAAAT  
 CAATAATCCGTGGCAACATATCTGTATAAACAAACACTGTAACCTCTAATAAATGTTTAGTCTTCCCTGTAAAA

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**FIGURE 36**

MLRGTM TAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGT VILGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQC VARMPAGAVASVPATVTL  
 ANLQDFKLDVQH VIEVDEGNTAVIACHLPESH PKAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQE VKTSGSSDRLRVRRSTAEAAARI IYPPEAQTI IIVTKGQSL  
 ILECVASGI PPRV TWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCMAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKQGAPAEAPI ILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWIPRGNGGFPIQSF RVEYKKLKKVG DWILATSAIPPSRLSVEITGLEKGT SYKFRV  
 RALNMLGESEPSAPSRPYV VSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMI IPASNNNT  
 PIHGFIYYRPTDSDNDSYKKDMVEGD KYWHSISHLQ PETS YDIKMQCFNEGGESEFSNVM  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL  
 IIVTFIPFCLWRAW SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTLPDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCCGLGLVPVEEVDSPDSCQVSGGDWCPQH PVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879



**FIGURE 37**

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTTCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
 AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCCAAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC  
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATTATGACGGGACT  
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT  
 CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
 TGCT**TGA**CACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

**FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS  
ALTTPGLTTPGTPTKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELV TSAEGLNSS  
QKLACLIGVXGGHSLDSSLSVLR SFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT  
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL  
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV  
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVR EESRAQSPVEAEFPYGQLSTSCH  
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTTQWLC

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146



**FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM  
PVPBGHDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE  
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGGACCCCAAGTGAGGGGCCCCGTGTTGGGGTCTCCC  
 TCCCTTTGCATTTCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGCGCCGCGTTGATG  
 CGGAGCAAGGATTCTGCTGCTGCCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCCAACTCAACTCCATCAAGTCCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA  
 AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA  
 GACCCCTGCCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAA  
 CCAGTGTCTCATCAGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTCTCATGGGCTGGAATTTTCCAGCGT  
 TGCAGCTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGGTGGAAAATAAGGTTGAGATGCAGAAGATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
 AAAGGGAGAAAAGAAAACATGAATGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATT  
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA  
 TACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAAACATGGAGCATTGTTAATTTACAACAGAAAAT  
 TACCTTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTCCAAATAATTGCAAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAAACAG  
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA  
 AACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAA  
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT  
 GATAGAATTAGATTGGTAAATACATGTATTACATACACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTATTTATTTTATAG  
 TGCTGAGATCCTCAAATAATCTCAATTTCAAGGAGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
 TTTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAAATTGTAAA  
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTCTTTGAAACCACTTTACTACTTTTTTTAACTT  
 AACTCAGTTCTAAATACTTTGCTGAGGACACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG  
 TAGACCACAATTCACTTTTGTAGTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG  
 AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA  
 CATTTTCTGCACAGGTCTGCAAAAACAAAATTATAAACTAGTCCATCCAAGAACCAGTTTGTATAAACAGGT  
 TGCTATAAGCTTGTGAAATGAAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATTTACAAT  
 TTGGTTTCTGCAATATTTTTCTTATGTCCACCCTTTTAAAAATTATTATTTGAAGTAATTTATTTACAGGAAATG  
 TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC  
 TTTGTAAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCCTCTAAAAACTGAAAAA  
 AAAAAAAAAAAAAAAAAA

**FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN  
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTTGGCCTCCCAAA  
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCCGGCCAACATCACGTTTTTAAAAATTGATT  
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
**ATG**TGTTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT  
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA  
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACACTACTACTTCTTGGGACCTCAAGCC  
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT  
CCTGGTTTTGGAGTCCTTTTCCTTCCCAGGCCAAAACCTTCGAGAATCAACACCTGGAGACAGTCC  
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG  
TCCACCAGCCACAGCCCCAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
AAAATAGTAATCAGATTCCCATCAGCTTGTATTGAAAGTCTTTAAGTGAGCCTTTGAATACA  
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG  
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC  
AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGTCCA  
GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
TGTGGAAAACACCAGTTGGTCAATGGCTCATTTCGT**TAAA**AAGCAGCCCTTTTGCTTTTTTGT  
TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAACAGTATGCAT  
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAAATCCCAGTGCTTTGGGGGGCC  
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC  
TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG  
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
GTCTGAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTSDWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSM TSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRI PYQSPVSSSESAP  
GTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24



**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTCACCGACGGCCCCCGGCCACCCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCCGG  
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA  
 CGGGCCCCCTTTTTCTGCGGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCAG  
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC  
 TGTCTCCTGGCCGCCCCGAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCCACCCCTGGCACAACC  
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA  
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
 CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGGCACCTGGGGCTGCACCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
 GGAATCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA  
 AAAAA

**FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRHVEEAQQVVHWDRQPPGVPHDRADRLDL  
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEPPIRGSPGNGSSHGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPLPAKYIDLKGFRENCK

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
ACTGCTTGAGAAGCTGCTGGACCGCCCCGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCT  
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT  
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
GGACCCTGAGGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTTGGCGTCACCATTGTCTGCATGGTGATCC  
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG  
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
AGGTACTACATGAGGCCTGTTCTTGGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
GGACTCCCTCAGTGCCCCCTTCGGTGGCCTCCAGATTCAATTGATTCCACACACCCCCCTCTCC  
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC  
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
GTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACTTTGCTGACCTAT  
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCCAACAGCAAGGCGCTCCCAGGG  
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT  
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
CTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCT**TAGA**AAGGGAGGACACAAGGACATTGGTG  
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
GTGAGCCACGTCCATGCCCATTCCTGCAAGGCAGATATTCCAGTCATATTAACAGAACACT  
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA  
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT  
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
AGTCCCCTGGCATGGTCAGTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
GCGGGTGAACAACTGCCCATAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT  
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
GTATTCAAAAA

**FIGURE 48**

MAVSEDDDFQHSSNSTYGTTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLA AHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITS LIYPAVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472

**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA  
 TCTCCACCGAGAGT**CATG**GCCCCATTGGCCCTGCACCTCCTCGTCCCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCCTCCCCAGGAAAAGGGCCACTCGCCCCAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGCTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG  
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA  
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTGCGCATGATTTTCTACCCGCCGC  
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCCGACGCGGCGGCAGCGTTCCGC  
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTCTGTCAGCGTTGGGCGGAGGACCAGCACA  
 GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT  
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGAAAAA  
 AA

**FIGURE 50**

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGC**AT**  
**GG**AGCCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
 GAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCT  
 GCTGCTGTTTACAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGTTTCCAGAAGAACAATGACCTAACAAGTTGCTG  
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
 ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT  
 CTGTCTCTTGATATAAGGTTATAAATCATCACCAGACCACTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCCAAAAGGCATTGGTGCTGAT  
 AGGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA  
 GCAAAGAGGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCA  
 AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG  
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATTGTTTCCCGGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCTT  
 GAAGAAGTTCTTGTGTAAGCTGGCTGTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATCTTGTCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTGGAGC  
 TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA  
 AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACGTTGGGGTGCCCTGGC  
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAATACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG  
 GCTTCACACAGGAGACATTGGTCTGGCTCCCGAATGGAACCTGAAGATCATCGACCGTAAAAAGAACATTTT  
 CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCACTGTTACA  
 AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTTCTGACACAGATGTACTTCCCTC  
 ATTTGACAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACCTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
 AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC  
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAG**GATAAGGTACTTAAGTACCTGCCGGCCCACTG  
 TGCACTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCTCCTATTTTTTTTTTAACC  
 TGTTAACTCTAAAGCCATAGCTTTTGTATATTGAGACATATAATGTGTAACTTAGTTCCCAAATAAATCA  
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
 GATCCCAAGTTTATGTTCTGTGTCCTTCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
 CAAAGGGACCCTCTGTGCCTTCTTCTTGTGTTTGTGATAAACAATACTTGCCAACAGTCTCTATGCTTATTTACA  
 TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATTCTGAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC  
 AAACCACTAAAAATTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
 CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGTATACACAAACATTTCTAAACTCTCTAGTTAGATA  
 TCTGACTTGGGAGTATTAATAAATTTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
 CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
 GGTGGGCCCCAGTGAACTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACTCCTGAACCTGGGAACAAAGATCT  
 ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGGATT  
 AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAAC  
 TATTACAGATAAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN  
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQERGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ  
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFELQKGIIRHDSFWDKLI FAKIQDSLGRVVRVIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSDGWLHTGDI GRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
SQPVLQIFVHGESLRSSLVGVVVPD TDVLP SFAAKLGVKGSFEELCQNQVVREAILEDLQKI  
GKESGLKTFEQVKAI FLHPEPF SIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622



**FIGURE 53**

GGAGGGCGGAGGCCGCGGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG  
 CCGGGGGCCCCCTAAGCCATTCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGCCGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA  
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG  
 AGGCCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCCCT  
 CAACATGGTAGCGCCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCTGTCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCAATTGCAG  
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT  
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG  
 TTTCCCGATCTTACCCTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACGAGGGCC  
 TACTTCAAGAAGCACAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGCCTTATGAAGTGAAGTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCCTGGTGGTGGGGGTCCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC  
 ACCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
**ATGA**GACCTCCTCCAGGACCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA  
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGAGTT  
 AAAAGTCTATTTATTTACTTCCTTGTTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA  
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGGCCGAACCTGGAGGGCCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA  
 GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT  
 GGTCAATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAA

**FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTVIVNIKLILDTR  
 RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
 REQGRGIHVIVLNQATGHVMAKRVFDTYS PHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK  
 DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS  
 AEEAECHWADTELNRNRRRRFCCKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
 RPNYLYRMLRSLLSAQGVSPQMITVFIIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY  
 KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLLEEDDSLYCISAWNDQGYEHTA  
 EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS  
 RSYHFGIVGLNMNGYFHEAYFKKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS  
 KNPCEDSFLPDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLVDVRGNHRGLWRLFRKKNH  
 FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC  
 CTGTTTAAAGAACCTAAGCACCATTTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA  
 AAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG  
 GTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA  
 GATATTCTTGAGGGAAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAAGCAGC  
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGA  
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCT  
 GGTTCCTGGGTTCCTCATCCCTCTCATCCTGTGCTAGGACACCAGCATTTAAATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC  
 TCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTTAAAACCTG  
 AGTAATGGAAAAGCTTTTAGAGTAGAAAACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG  
 GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAAGCTATGTCTCTTTCTTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT  
 AACATGGTTCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT  
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAAT  
 ACCTGTCTCCACATTCTTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTTCCTTCAAGAA  
 CAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTTTAAAGTGATTTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAATGTATGGTTGTCTTTTTTTTTTTGTTTT  
 TTTTTTTTTTAATTATTTCTTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT  
 GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA  
 TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCTCTTTCTTTGCTTTTCTTTCTAACTTT  
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAATT  
 CTTATCAGGACAACCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTCTTTATCCCCCTT  
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATAACCACCTCCTCATGTGTAA  
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAGTGTTAACAGACTAGGATA  
 ATTTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGATATAATATTGTAT  
 TATTAATTTATTTTTACTTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG  
 ATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA  
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCVAGIIP LAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTTGLVVHAAADGVALGAAASTSQTTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLV FALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIP LILSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

56/249

**FIGURE 57**

GCTCGAGGCCGGCGGGCGGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA  
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA  
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCTTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCCTACGACCTGAGCCAGTGATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAA  
 GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
 CCAGGCCGGGAGCAGGTGGTGGAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGCTTGTTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA  
 TAAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA





**FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW  
 MASRFSRVVLVLIDALRFDFQAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ  
 VDPPTTTMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF  
 PGAFSKAFFFPNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHHPPEM  
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST  
 PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAEFSGGEDSQPHSSALAQAASALHLNAQ  
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
 ARAMCIESWARFSLVRMAGGTALLAASCFICLLASQWAI SPGFPPCPLLLTPVAWGLVGAIA  
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLFRLA  
 VFFSDSFVVAEARATPFLLGSFILLLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY  
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA  
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMLVP  
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
 EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
 LLHLLAAGIPVTTGPGFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAFFVGFPEGHGS  
 CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQPPGNEADARVRPEEEEEEP  
 LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFIFEAVG  
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
 1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271



**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT  
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA  
 GATTCTTTGTGCCTGCTGAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT  
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCC  
 CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC  
 AAACCTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAC  
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
 TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG  
 TGGGTGT

**FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED  
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYEDVRTTDICAGPEEQELSL  
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPPSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGCTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGGCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAGAAA

**FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLLTLMCTRS GDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**

amino acids 1-30

**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG  
 CAGGCGCCGCGTGTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTCGCCATCGTCCCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAACTGGCGGATGTT  
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCCTCCCCAG**TAA**CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTGAGGGCTTCCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTATCCC  
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACAGCTGCTGCTACAGGACCTGGGA  
 TTGCCTGGGACTCCACCTTCCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAC  
 TTGCTCATT

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVLDILINN  
AGVMRCPHWTTEDGFGFEMQFGVNHLGHFLLTNLLLDKLGKASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW  
AESARLVGLEAPSVREQPLPR

**Signal peptide:**

amino acids 1-17

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**FIGURE 67**

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGTCAT  
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCACGTGGTAGC  
 TGAGGCTGTCACTCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTCAGACCCTGGGTTCCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT  
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA  
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTACCAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC  
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGGAAGTTTCTGG  
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC  
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
 ATGTTTATAAATCAAAA

**FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19



### FIGURE 69

[illegible]

**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL  
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGV PYTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDV IYVRGCTNAVI IWFMDNYTIMACILLGILLPQFLG  
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

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**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC  
 TTGATCCAAGCCACCCTCAGTCCCAGTTCATCCTCGGCCCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAAGTGTGCTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC  
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTTC  
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC  
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG  
 ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA  
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAAACACTTGCCTGTGAAAAA

**FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDHNATSILQQPLLSAM  
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGD TIQLYL  
GAKLLDSQGGKVTKWFNNSAASLTMP TLDNIPFSLIVSQDVVKA AVA AVLSPEEFMVLLD SVL  
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL  
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGW FQPDVLKNIITEIIHSIL  
LPNQNGKL RSGVPVSLVKALGFEEAESSLT KDALVLT PASLWKPSSPVSQ

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
CTCATCGTTTTCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
AGTTCGGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
CTCCAACCTGCATAGACAGTGTGTGTTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCATGGTGGATTTTG  
ATGAAGGCTCTGATGTATTTAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT  
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTTCAGC  
TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTTGCAGCTTTGTG  
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC  
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGGCTTTTATG  
TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTTAGATCTAAATATCATGGCTAC  
CCATACAGCTTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
ATTGAAAACGAAAATCGTGTGTGTTGAAAAGAAGAATGCAACTTGTATATTTTTGTATTAC  
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAAGAAGATGTGTAGTGCCTTA  
ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA  
CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACCTACTTTAGTTAACTTGGTCATCTGAT  
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCCATATATGCC  
TGTTACAGATAACTACATTAGGAATTCATCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGCATGTGGTCTTCTGAAAATG  
GAACACCATCTCTCAGAGCACAGCTTAGCCCTCAGCAAGACAGTTGTTTCTCTCCTCCTT  
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA  
GATTTAGATTTCATTCCATCTCCTTAGTTTTCTTTTAAGGTGACCCATCTGTGATAAAAATA  
TAGCTTAGTGCTAAAATCAGTGTAACCTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC  
GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
AGCCTGGCAACAGAGCGGAGACTCCATCTCAAAAAAAAAAAAAA

## **FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRNPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

**FIGURE 75**

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA  
 GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCG**ATG**CTA  
 CTGCTGTGGGTGTCGGTGGTCGCAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA  
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGCTGGTCGTGAGCGACTCCTTCGATG  
 GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG  
 ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC  
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGAATAATTTTAAGGGTCTAG  
 ATCCAAATTATACAACATGGATGGATGTATGGAGAGGCATGGCTACCGAACACAGAAATTT  
 GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG  
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAAACAGGA  
 CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAACTGGTTAAGA  
 AAGGAAGCAATTAATTACACTGAACATTTGTTATTTACTTGGGATTAAATTTACCACACCC  
 TTACCCCTTACCATCTTCTGGAGAAAATTTTGGATCTTCAACATTTACACATCTCTTTATT  
 GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAGAAATG  
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAACTGCACTGGAAGATTTACAAAAAAGA  
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG  
 AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACCTATTGTCATATACTCCTCA  
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG  
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAAGCCGGCCTACAAGTATCAAATG  
 TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG  
 AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAAGT  
 CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA  
 CCTACATGCTTCGAACTAACCACTGGAAATATATAGCCTATTTCGGATGGTGCATCAATATTG  
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCC  
 AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG  
 CTTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT  
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA  
 TGAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA  
 GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT  
 AAATGAAACAGTTTTAATAATTACCAAGTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC  
 CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC  
 CAACATGGTGAAACCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA  
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG  
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCGC  
 AAAAAAATAAAAAATAAATAAATAAATTACCAATTTTTTCATTATTTTGTAAAGATGTAGTG  
 TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAATGGTTATTATTTA  
 GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAATACTGTA  
 ACAGTTATGTTCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAT  
 AGTTGTATGTGAGCATTTGATGGTGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINF  
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLGILNLPHPYPSPSSGENFGSSTFHTSLYWLEKVSFDAIKIPKWSPLS  
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS  
ILPQLFDLSSDPDELTVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97



**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC  
 CAGAGAAATCGCTCCAACTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT  
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG  
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG  
TGAAGCTGAAGGTTTCAGGGTGTGAATTTCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCC**TGA**GAAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

## **FIGURE 80**

MVPRIFAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

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**FIGURE 81**

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTCGCAGTGTGAGCT**TAA**TGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT  
CTGTGACCTGTCTGAGGCCCCACCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

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**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAGTTCCCTCT  
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG  
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCCAAAGATGCACCATCCAAGTGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCCGTGCCCAGGAGCTGGTGC GGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTTGAAGCCTCACACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCCTG  
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTTCGGAGCCCAGCAC  
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
 CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCCTGTTCCAAGGATTTTGGGGTGCTGAG  
 ATTCTCCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGGCACGGTG  
 GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC  
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK  
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLTLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216





**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPEKVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 87**

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC  
GTGGGCGCTCCGCTGGCTGTGCAGGCGGCC**ATG**GATTTCCTTGCGGAAAATGCTGATCTCAGT  
CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG  
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG  
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA  
CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTCACCG**T**  
**GA**GACCGGACTTGCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC  
TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG  
TCCTGTGAGCTGCCGTGCGGTGAGCACGTTTCCCCCAAACCCTGGACTGACTGCTTTAAGGT  
CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAAACCAATAAAA  
TCATGTTCTCCAA  
AAAAAAAAAAAA

## **FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

**Signal peptide:**

amino acids 1-18

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**FIGURE 89**

[illegible]

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVRVFPWVG TGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTQ  
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAAGTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTTCTCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATCTGAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGGACTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACTCCC  
 ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSY YQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTD SRTN RDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAE LDWRRKHGQAE LRDARKHAVEVTLD PETAH PKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGH NKRWRVGVC RDDVD R RKEYVTLS  
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNS ESSSQATT PFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255





**FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRS LPS L GGLALLCCAAAAA VASAASAGNV TGGGGAAGQVDASPGPGLRGEP SHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTVPVATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTTCATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTC  
CACAGCA

## **FIGURE 96**

MGGLLLAAFLALVSVPRQA VVLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC  
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
CCGCTCCTCGGTGCTCACCCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
ATTACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG  
GTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTTCAGCCT  
CTCAGGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
ACAGATGAAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA  
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
CCACACTGTGCCCTCCCTTTTATTTTTTTTAACTAAAAGACAGACAAATTCCTA

**FIGURE 98**

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPQNLTMVTFQGDG  
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDTGIEDANAVRGSSAQGPLTEPWAEDSPDQPPPASARSSVGEGELQYA  
SLSFQMKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

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**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTTCCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

## **FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

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**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAAGGGGAGAGACCAGGATCATCAAGGGGTTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT  
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTTCTCTGTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITW  
AVRPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLR CANITII EHQKCENAYPGNITDTM  
VCASVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTTAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCCTATGAGAAGATATTTTGA  
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLGWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDDLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDIFKKNDHGDGDFISPKEYNVYQHDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

**FIGURE 105**

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

## **FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL  
ETCNARHGGSRL

**Signal peptide:**

amino acids 1-18

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC  
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**  
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACCT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

## **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17



## FIGURE 109

CGCGCCACACGCAGCTAGCCGGAGCCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTTGA  
GGACCCCGCCTGGACTCCCCAGCCTTCCACCCCATACTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTGTGTTGGTCATTGAGGGTTTGTTTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC  
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCACCC  
AGGACACAGCCACTCGGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGACAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAAGTGAGGCCTG  
GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGCTGTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

110/249

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGACAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCACACC**ATG**GCCCCCGGGTGGGCAGGGGTTCGGCGCCGCCGTGCGCGC  
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTTGAGTGGGCCTCCAGCCGTGCGCTGCC  
CACCAAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTT  
CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACT  
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT  
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGATCCTGGTCACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTTGGCGCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTTACACTCT  
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTTGCCA  
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA  
AGATCACCGAGATTGCCAAGGGACTGTTTGTATGGGCTGGTGTCCCTACAGCTGCTCCTCCT  
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCTCTGCGAGT  
CCATCCAGACACTCCACTTAGCCCAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCCGCGCCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTTTCAGAGCGAGTGCTTCAACACAGAAGCTGGTTCGCGATCCCAAGCCACCTCCC  
TGTGAGGGCACGATTGTGACTGCTTCAACACAGAAGCTGGTTCGCGATCCCAAGCCACCTCCC  
TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT  
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTTCGGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTAGGTGCCAGAAGCCATTTTTTCTC  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCTTGAAGG  
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTC  
TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
ACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC  
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATG  
AGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG  
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGCCAGTG  
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG  
AACACCCCCCACCCTATGGTCCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC  
GGGGCCAGTGCGATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG  
CCCCAGATGCGAGAAGCTCATCTGCTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGG  
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
GGCATCCTTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAGGGCCACGT  
GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA  
ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG  
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG  
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCCCTGCACCGT  
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
GCTGGACCGGCCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
CATGGAAAATGTGTGGCAACTGGGACCTCATACTGTGCAAGTGTGCCGAGGGCTATGGAGG  
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG  
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGCT  
GTGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG  
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC  
**CTAA**GGCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
ATGTGGGACCCCTGGTGATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAA  
AAAAAA

**FIGURE 112**

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLKNKLQVL  
 PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGA FRALRDLEIL  
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
 RGENVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
 GLFDGLVSLQLLLL NANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
 AQNPFCVDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIRSRFS  
 SECMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
 SNDTFAGLSSVRLLSLYDNRI TTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR  
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR  
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDL SNNSISMLTNYTFSNMSHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCDSLRLW  
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKCNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR  
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLQHEAKCIP  
 LDKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPMV  
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS  
 VELVTNLNQLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGA AAAAAGGCTGTGAGGTTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCTCCCAATA  
TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

## **FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDALICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

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### FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT  
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCC  
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCCAATTGACTGGATAGAGGAATAC  
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG  
CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTCTGC  
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTTCATCTGATCGTGGCAGGTGG  
TTATGACGAGAGAGTCTTGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC  
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
TCTGGAAGCCATGTACATGCAGTGGCCAGTCATTGCTGTTAATTTCGGGTGGACCCCTTGGAGT  
CCATTGACCACAGTGTACAGGGTTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA  
ATAGAAAAGTTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
AGTGAAGGAAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  
TGCTGGTATAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTTATGGATTGTAGACC  
CAGTTTTGAAACCAAAAAAGAAACCTAGAACTAATGCAGAAGAGATCTTTTAAAAAATAAA  
CTTGAGTCTTGAATGTGAGCCACTTTCTTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
AACCATGTCTTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA  
AGTTGATTAAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT  
CCACCGAAGTGTTCACTGTCTGTTAGGGAAATTTTTGTTTGTCTGTCTTTGCCTGGATC  
CATAGCGAGAGTGCTCTGTATTTTTTTTTTAAGATAATTTGTATTTTTTGCACACTGAGATATAA  
TAAAAGGTGTTTATCATAAAAA



**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLARRRKKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVP EKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSSGGPLESIDHSVTGFLCEPD PVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

## FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT  
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAATGGTGT  
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGTCT  
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCTAC  
TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTTCATTGACTC  
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
CCAGTTGCATAATAACTGCAAAATTTGTGTACCTGGGCAATCTGTTTTTTTAACCACCTCTGAA  
GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTTTTTGAAATGGTCCTGTTACTCC  
AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTCTGAACTGCCA  
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT  
CCTAGAGAGACCCTCGTCCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT  
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
AT**TAA**AATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA  
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
TTAA

**FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLLVSVLGTVDVLKQHINPNKTSDFPFETMLKSLLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG  
TGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA  
AAGAAACCCTTCTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTTAGGGGACA  
ATTAAAAAAAAAAAAA

## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACT**ATGT**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC  
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TG**AGGCC  
CTGCTGATCCGCACCCCATTCTCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

**FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNVMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

## FIGURE 123

CTGGGACCCGAAAAGAGAGAGGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
GACTCGCTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
CGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
CCTAGGGCTGCTGGCCCCGCTTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC  
GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATC  
TGGG**TGA**CCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
CTGGTCCCAACCTGAAGCTGTGGAGTGA CTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG  
GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC  
ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCCTC  
CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGAG  
GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTTGT  
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT  
GCCCCGGGGCA



**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY  
YPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 125

GTGAATGTGAGGGTTTGTATGACTTTCAGATGTCTAGGAACCCAGAGTGGGTGCAGGGGCCCA  
GGCAGGGCTGATTCTTGCGGCGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG  
CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
GGCTGCGGCTGCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGGTAAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCAA  
GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG  
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTCCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGGAAGATCATTTTTTTCATCATTTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCCTTTGGAATTAGTTTGTTTGTTTCTTGTA  
AAAACCTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
TGGCTTGCCCACAAATTTACCTTGACTIONGATATCATCGACATGACTTCTCTCAAAAAAAAA  
GAATGCTTCATAGTTGTATTTTAAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC  
TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTTT  
TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA  
TTAATATATGTTAAAAAAA

## FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSNPATDSKGSSSSPLGI  
SVRAANSKVAFAVAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLSEVVFVAPRKGIIYSFSF  
HVIKQVQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

**FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLG  
GIMSGVFSFVNTLSDSLGPSTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDGCEKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKLCLLCQDKN  
FLLYNQRSR

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTGCTCTGGGCTTGCCCTTCT  
 TGGTGCTCTTGGTGGCTCGGTGCGAGGCCATCTGGGGGTTCTGGGGCCCAAGAAGCTCTCGCAGAAAGACGCCG  
 AGTTT**GAGCG**CACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC  
 GCAACAGGACAGAGGGCGTGCGTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG  
 TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT  
 ACCAAAAAGTGGAAACGAACCTGTGTACGCCCCCACCAGAAGATGAGTCGGAGATT**CAGT**CTTCTACGTGGATG  
 TGTCCACCCCTGTCAACAGTCAACACCACATACAGCTCCGGGT**CAGCCGC**ATGGACGATTTTGTGCTCAGGACTG  
 GGGAGCAGTT**CAGCT**CAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCTGAAGCGTGGACT  
 CGGTAATTGTCAAGTGACCTCCAACAAGGCCTTCCCCTGCTCAGTCATCTCCATTCAGGATGTGCTGTGTCTCTG  
 TCTATGACCTGGACAACAACGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC  
 AGCGCAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT  
 CCCTGCTTTTCTACCCCTTCGAGAAAGATGAACCGGTGCATCAAGGGCACCGCCAGAAAACCTGT**CAGT**CTGG  
 TGTCTCAAGCAGTCAAGCTCTGAGGCATACGT**CAGT**GGGATGCTCTTTTGCCTGGGTATATTTCTCTCTCTTTTACC  
 TGCTGACCGTCTCTTGGCCTGCTGGGAGAACTGGAGGCAGAAGAAGACCCCTGCTGGTGGCCATTGACCGAG  
 CCTGCCCAGAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCCCTTATGAGGGTTACAACCT  
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG  
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG  
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGT**CATT**CGCACCAGCAATACCTCTATGTGGCTGACC  
 TGGCAGCGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGTCTGTCT  
 TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT  
 GCTACTACAACCTCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT  
 ACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA  
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA  
 TGGAGGGGCTGCTCAGTCTTGTATCATGTGTGCCCCAACTATAACCAATTTCCAGTTTGACACATCGTT**CAT**GT  
 ACATGATCGCCGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG  
 CCTACGCCTGCCTGGCCATTGT**CAT**CTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTTCT  
 GGATCGTCTTCTCCATCATT**CACAT**CATCGCCACCCCTGCTCCTCAGCACGCAGCTCTATTACATGGGCCGGTGGGA  
 AACTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC  
 TCTACCTGGACCGCATGGTGTGCTGGT**CAT**GGGCAACGT**CAT**CAACTGGT**CGCT**GGCTGCCTATGGGCTTATCA  
 TGGCCCCCAATGATTT**CGCT**TCTACTTGTGGCCATTGGCATTCTGCAACCTGCTCCTTTACTTGCCTTCTACA  
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT  
 GGGGCTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCAGGGGAGCACA  
 ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTT**CG**  
 GGTCTTCTGCTGTTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTT**CAGC**  
 AGGAGCTGGGCCCTTCGCTTCAACCTCAAGGGGCCCTGAGCTCCTTTGTGT**CAT**AGACCGGT**CAT**CTGTCTGTGCT  
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT  
 GGGACAGCCATGGGGTGGCATGGAACCTTG**CAGCT**GCCCTCTGCCGAGGAGCAGGCCTGCTCCCTTGAACCCCC  
 AGATGTTGGCCAAATTGCTGCTTTCTTCTCAGTGTGGGGCCTTCCATGGGGCCCTGTCTTTGGCTCTCCATTT  
 GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCCTCCCCATTT**CAT**GCCTTGCATTTTGGCCGCTCCTCCCC  
 ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCCCTACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA  
 ATCTCTGCTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCCATTCAGT**CAGCC**  
 AGGATGGATGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGG  
 CCTGGGGCAGTGCGTATTCTTCTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCCAAT  
 TGAGAACC**GCCT**TCTGATTCAAGAGGCTGAATT**CAGAGGT**CACCTCTT**CAT**CCCATCAGCTCCCAGACTGATGCC  
 AGCACCAGGACTGGAGGGAGAAGCGCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCC  
 AGCTGGTGGCCTTT**CAGT**GCCATTGACACTGCCCAAGAATGTCCAGGGGCAAAGGAGGGATGATACAGAGTT**CAG**  
 CCCGTTCTGCCTCCACAGCTGTGGGCACCCCACTGCTACCTTAGAAAGGGGCTT**CAGGA**AGGGATGTGCTGTTT  
 CCCTCTACGTGCCAGTCTTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTT**CAGGCA**  
 AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC  
 CTGGCCACCC**TGGT**CTTGGATCCCCTTCTGCCACCTGGTCCACCCCAAGATGCTGAGGATGGGGGAGCTCAGG  
 CGGGGCTCTGCTTTGGGGATGGGAATGTGTTTTTCTCCAAACTTGTTTTTATAGCTCTGCTTGAAGGGCTGGG  
 AGATGAGGTGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT  
 TGCATTCAATAAACCAACCAGACTCAAAAAAAAAAAAAA

**FIGURE 130**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT  
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE  
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSVI  
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVFIGMYQTMKKAAITVQRKDFPSNSFYVVVV  
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLSVLVSQAVTSEAYVSGMLFCLGIFLSFYLL  
TVLLACWENWRQKKKTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL  
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL  
ARKDKRVLRRKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYYNFLCAHPLGN  
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM  
MEGLLSACYHVCPNYTNFQFDTSEFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS  
VLGVVFGKGNTAFWIVFSIIHIIATLLLTSTQLYMGWRWKLDSGIFRRILHVLYTDCIRQCSG  
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI  
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFFDDHDIWHFLSSIA  
MFGSFLVLLTLDDDLDTVQRDKIYVF

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCTCAAGTGGCCTGCCCTITGCCCCACCCAGCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTG  
 ACC**ATGG**TCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC  
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA  
 GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
 CTTCTCTTCCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC  
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT  
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
 AGCCGGCTCTTTCCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCTCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA  
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
 CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTCGCTGCAAC  
 GTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTCGGC  
 AGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCCCTCATCCTCATTTTTACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG  
 ACTGTCT**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGCCCAATAATAAAGCCCCA  
 GAGAACTGGGCTGGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG



**FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIIESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPRLAGQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE  
GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLLTIQSPDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTALHWWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGAC**ATG**AGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTTCAGTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCGTGAGGCGGCCGCCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTCCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGCGGGCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC  
 TTCTCCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GCGATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG  
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC  
 AGCATCACCCCTTCCCTGGGTGGCATGTCTCTCTCTACCTCATTTTTAGAACCAAAGAACATC  
 TGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT  
 TCGCAGTCTTCTGGAAAATATTTTCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGTC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCA  
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTTCAGGCTGGTCTCAAACCTCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCGCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCACATCTGTCCTAATGGGCTTACCTCCT  
 CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT  
 TCCTTGTCTGGTTTG  
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT  
 GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCCTTTTGTGTGTGTGTGTGTGTGTGT  
 TTGTTTTTTTGTCTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

**Signal peptide:**

amino acids 1-16

## FIGURE 135

[illegible]

**FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

### FIGURE 137

[illegible]

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVPVSSIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCC**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTTGTGAATAAACTTGATACACCA



**FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

141/249

**FIGURE 141**

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC  
 CCCGCGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG  
 GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGCGGGACACCGTC  
 GCTCCTGCTCTCCGAATGCTGCGCAACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCCATGGGGCGCGCTGCCG  
 CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGTCAGCCGCCGCTCCGACCTGGGCGCTCAGC  
 CCCCAGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCCCTCAGATTGGAAGCTGAACACATCTCCAACCTAC  
 ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC  
 AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGTGTCAGACGCAGAGAAGAAACAGCAGTGC  
 AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC  
 CTGTTCACTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCCTGGCAAGG  
 GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC  
 CTGGTGGTTGATGGCGAGCTTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC  
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC  
 ATTCCTGAGAGCCTGGGCAGCTTGAAGGCGATGATGACAAGATCTACTTTTTTCTTCAGCGAGACTGGCCAGGAA  
 TTTGAGTTCTTTGAGAACACCATTTGTGTCCGCAATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
 CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCCGACGATGGCTTCCCCTTCAAC  
 GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCTTTTCTATGGGGTCTTCACT  
 TCCCAGTGGCACAGGGGAATACAGAAGGCTCTGCCGTCTGTGCTTTCACAATGAAGGATGTGCAGAGAGTCTTC  
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG  
 CCTGGAGCGTGCATCACCAACAGTGCCCGGGAAGGAAGATCAACTCATCCCTGCAGCTCCCAGACCGCGTGCTG  
 AACTTCCTCAAGGACCACTTCCTGATGGACGGGCGAGTCCGAAGCCGCGATGCTGCTGCTGCAGCCCCAGGCTCGC  
 TACCAGCGCTGGTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGCGGCACTGGTGAC  
 GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGGTGACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA  
 CAGCCCGTGCAAGATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG  
 TGCCCCATGGCCAACCTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCCGGACCCCTACTGTGCTTGG  
 AGCGGCTCCAGCTGCAAGCACGTGAGCCTCTACCAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG  
 GGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCGTCTTTTGTACCAACAGGGGAGAAGCCA  
 TGTGAGCAAGTCCAGTTCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA  
 CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG  
 GTGGGCACCCAACAGCTGGGGGAGTTCCAGTGTGCTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC  
 TGCCCCAGAGGTGGTGGAGGACGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA  
 TCGCGTGTGAGTGCACCAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTTGGTG  
 ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA  
 GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC  
 CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG  
 GGGGCCCCAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG  
 TGCCCCCGGGCCCGGTCGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC  
 TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCCTCCGCTCTGCTCTTCGTGGAAC  
 ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC  
 TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCCTAGGTTGGTGGAA  
 CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAACAATTCAAATGTGAACTAGAATGAGAGGGGAAGAG  
 ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG  
 TTGCTGAGACAGAGTTGGAAACCCCTCACCAACTGGCCTCTTCACTTCCACATTATCCCGCTGCCACCGGCTGC  
 CCTGTCTCACTGCAGATTGAGGACCAGCTTGGGCTGCGTGCTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG  
 TTGCTGCCGTGCTCCACCACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC  
 GGACCCAACTCCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA  
 TTTCTGTACAATGTACGCCTTTCCCTCAGAATTCAGGGAAGAGACTGTGCCTGCCTTCTCCTCGGTTGTTGCGTGA  
 GAACCCGTGTGCCCTTTCCACCATATCCACCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTCAACC  
 CTGGTCCCTTCCCCAGTCCCCAGTTACCCCTCCATCCCTCACTTCTTCACTCTAAGGGATATCAACACTGCCC  
 AGCACAGGGGCCCTGAATTTATGTGGTTTATATACATTTTTTAATAAGATGCACCTTTATGTCAATTTTTTAATAAA  
 GTCTGAAGAATTACTGTTTAAAAAAAAAAAAA

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP  
FDPNFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSlyQP  
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLLLVGTTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVVIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA  
GCCACGCCAGCCGAGGACGCGGCGAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGTGTCGCCCGTCG  
TGCCGGCCCCCGCTCCCCGCGCGCAGCGGGAGGAGGCCGCCACCTCGCGCCGAGCCCGCGCTAGCGCGCGC  
CGGCGATGGTCCCCCTTTAAAGCGCAGCGCGCGCGGGCGGGGTGTGCGGAACAAAGCGCGCGCGGGG  
CTCGCGGGCGGCTCGGGGGCCGCGATGGGCGCGCGCGGGCCGCGCGCGCGCGCTGCCCGGGCCGGGCTCG  
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGCGGCGGC  
GGCGGCGGCGGCGGCCCGCGGGCGGAGCGGCGCGGGC**CATG**CGCGCGCGGCCGGCGCGCCTGGCTCAGCGTGC  
TGCTCGGGTCTCTCTGGGCTTCTGCTGGCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG  
GCCACGGCGCGCGCCAGCCCCAGGGCTGCCGTCGGGCGAGCGCGGCTTCCAGCGCGCGGGCGCGCG  
GCGATGCGCGCGGGCGCGAGCTTGGCCGCCCGCTCGGACCCAGATGGCGCCCGCGCAGGAACCTTCTCT  
TCGTGGGATCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAT  
TTCTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGG  
GTGTGGACGACTCTACCCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCCTACTTGGACA  
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAATCTCTGAGGAGTT  
TGAACAGCAGCGAGCCCTCTTTCTTGGGCGAGCAGGCCCTGGGCACCACGGAAGAAATGGGAAAACGGCCCTGG  
AGCCTGGTGAGAACTCTGCACTGGGGGGCCCTGGCTGATCATGAGCCGGAGGTGCTTCGGAGAATGGTGCCG  
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG  
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAGGGT  
ACATTAGAGATCTCCATAACAGTAAAATTCACCAAGCTATCACATTACCCCCAACAAAACCCACCTTACCAGT  
ACAGGCTCCACAGCTACATGCTGAGCCGAAGATATCCGAGCTCCGCCATCGCACAAACAGCTGCACCCGCGAA  
TTGTCTGATGAGCAAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTCA  
TGAGTCTTACGCCCCCAGCAGAGGAGATCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTCCGCG  
TTGACGGCCAGCCCCCTCGAAGAGGAATGGAATCCGCCCAGAGGGGAAGCCTTGGACGACATTGTATGCAGGTCA  
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
GGGTGAACCCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTCTGTACAAAAGCACAAAGGGAAGAAAA  
TGACGCTCCCTGTGAGGAGGACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
TGGATGCACAAGAGTTGGCCAAAGAAATCAATCAGGAATCTGGATCTTGTCTTTCTCTCAAACTCCCTGAAGA  
AGCTCGTCCCTTTTCACTCTCCCTGGTTCGAAGAGTGAGCACAAAGAACCACAAAGATAAAAAGATAAACATACTGA  
TTCTTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC  
AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATCTGACTCCAACCTTGACAAGGCCAAACAAGTTGAAGTATGA  
GAGATTACCGCATTAAGTACCTTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTTCAAGAGCCCTGG  
CCCTGGAAGTAGGATCTCCCACTTTAAACATGAATCTTTGCTCTCTTCTGCGACGTGCACCTCGTGTTTACTA  
CAGAATCTCTCAGCGATGTGAGCAAAACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTCTCAGCCAGT  
ATGACCCAAAGATTTGTTTATAGTGGGAAAGTTCCCAAGTACAAACATTTTGCCCTTACTCAGAAAACCTGGCTTCT  
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA  
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC  
AGGAAGTAGGAGTAGTCCACGTCACCATCTCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT  
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
GTTACAGTAAAGACGACAAATAATAATGGCTCAGTGAGGACAGCC**TAAAT**CTCCAGCTTGTCTGGAAAAGACGTTTT  
TAAATTATCTAATTTATTTTCAAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC  
AAGTGGTTTTCTTACATAGGACTCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA  
CACATCTTCTGTGAACATTATGTAGCAGACCTGCTTAACCTTTGACTTGAAATGTACCTGATGAACAAAACCTT  
TTTTAAAAAATGTTTTCTTTTGAACCCCTTGTCTCCAGTCCATGCGCAGAAAACGTGAACATCTCTGCAAGTAT  
TATTTGTAACAAAACATGTAACTGTGTAATGTTCTGTTGATTTGAATTTCAACATCCACAGATTCTACCTTTTGT  
GTTTTGTTTTTTTTTTTCAACATTTGTTTTAAAGCCATTTTCATGATTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
GCTGTTTCATCATTTGTCTTCAGGAGAGCTTTCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC  
CACGTAGGTTTTTTTTGTTTGTGTTTTGTTTTGTTCTTTTTTTGAGACGGAGTCTCACCTCTGTTACCCAGGCTGGAATG  
CAGTGGCGCAATCTTGGCTCACCTTTAACCTCCACTTCCCTGGTTCAAGCAATTTCCCTGCTTTGCTTCCCGAGT  
AGCTGGGATTTACAGGCACACACCACCGCCAGTATGTTTTTTGATTTTTTAGTAGAGACGGGTTTACCATT  
GCAAGCCAGCTGGCCACGTAGGTTTTTAAAGCAAGGGCGCTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG  
TGGTAGTTTCAATTCGGCCTAAATAGACCTGGCATTTAAATTTCAAGAAGGATTTGGCATTTTCTCTTCTTGACCCCT  
CTCTTTAAAGGGTAAAAATATTAATGTTTGAAGTACAAAGATGAATTTATTAACAATAAATCTGATGTACACAGACT  
GAAACATACACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTTCATCCTGTCTGT  
TGTTATGTGGGTGGAGATGGTTTTTCATTCTTTCAATTAATCTGTTTTGTTTTATCTTTTGTATCTGAATACCTTTAA  
TTTTTTTAAATATCTGTTGTTGACAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG  
GAGTGTGTTTTAGTCTGTTTTTATTTGAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTTTCCCTCC

**FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG  
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTGGAATAAACCAGTGAACAATATTTTCTATTGTACTTTTGAACCATTTTGTCTCATT  
ATTCCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAACTTAAACACGAAAAA

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT  
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE  
ILEWEFLTGTKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNP MYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKVVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGACGACGCCT**ATGA**AGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT  
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA  
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC  
TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA  
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAAATAAAATTTTGGTTCAGGAAAAAA

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTTFPTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAEOPYIENEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19



**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACA  
 GGAATATCC**ATG**GCTTTTTGTGCTCATTTTGGTTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGC  
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCAGC  
 CCACAGCCAAGTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA  
 GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCCGGAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACAATGTG  
 ACTTTGTCTCCCAACAATGGGTATTTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC  
 ATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATAACC  
 CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTTGGGGAT**TC**GAGACAGAGAAGACCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC  
 CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCCTCCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTTGCCTCACAGGTGAAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGTTTGCTAATGATGTGTTTTTA  
 TATTATACATTTTCCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA  
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
 GAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAACCAGGCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
 TTCTAAATAAAATTTTAAACAAATTAACTAAACAATATATTTAAAGATGATATATACTACT  
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAATT  
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC  
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDVRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

### FIGURE 149

CCTTACACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCGTCAGATGTGGTGAGGGGCTA  
GGAAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA  
TTACTATAGCACATTGTCAATTTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
CTAACAAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTATCAAGTTCAGTCAACAGAAGCATGG  
AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
ATAAAATTGTTCAACTTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
GATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG  
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCAGATGACTATGATATTTCT  
CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAG  
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT  
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
TGTTTGTCTTGATGCATGTATTTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAC  
TTGTTGACATAAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
AGCTCCTCTCATTTTCAAGCAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA  
TAAGAAGAAAAAATCCCCTACATTTTATTGGCAGAGAAAAGTATTAGGTGTTTTTCTTAGT  
GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
TCCTTATTTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAAGCAAATAT  
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

**FIGURE 150**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD  
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR  
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL  
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG  
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV  
MFVTGFGALKNDGYSQNHLRQAQVTLLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD  
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 151**

GTCTGAAGGTTATAAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCCG  
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTTCGGGCCGGCGGCCTGCCTGTGCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCTCCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAACCTGAAGGGGCTGAAGCCAGGGGGCATTTATGTCTGTTTGCCTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
CCTGCCTTCGGGCCTTGACAGCCGCCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC  
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**  
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA  
AGCGGCCAGATAATAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLC PGLSSPAQPPDP PRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA  
AQKGPPLNATVRR AELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTL VHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

154/249

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
CTGCCCCGATGAGCCCCCGCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG  
CCCAGCGCCGACGATCGCTGCCGTTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGG  
TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA  
TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
ATTTTGACTTACTTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCTTATCAT  
TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT  
TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
GAACTTATGTTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA  
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTTTCAGAGAGAGTTTAAAGT  
GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT  
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCTTTTTTGAGAGGAACCAAACTGC  
AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC  
CTTGAAGAATGACAACTCTCAGCACCTGTCTATGTCCTCAGTAGAACTGTTGAAACCAAGCC  
TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG  
GAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT  
TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA  
CCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC  
CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTT  
CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT  
CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
ACTTTTATTACTCAGCGACTATTTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTC  
AATATTGGTGACTACCTAAATGTGATTTTGTCTGGTTACTAAAATATTCTTACCACTTAAAA  
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTAA  
TCTGTATAATTTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTTGAAAAGGAAA  
ATTTGTCTGTATAGCATCATTATTTTTTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGT  
CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA  
CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
GAAAATTTGCACATAACTTAGTTGATTTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG  
AAGACTCTTTTTTGACACTAAACACTTTTTTAAAAAGCTTATCTTTGCCTTCTCCAACAAGAA  
GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTTCTCCAGAAAAAT  
GCTTGTGAGAATCATTAACACATGTGACAATTTAGAGATTCTTTGTTTTATTTCCTGATTA  
ATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTTACAAGAGTATAGTATATTTATTT  
GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAA  
AGAAAATTAATAATGTGTCAATAAATATTTTCTAGAGAGTAA

**FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ  
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTENDWPPDSCCVREF  
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



## FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGGTGATTCTGGATAAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGA**ACT**GGTTCTCTGCCTGTTTCGACA**ACT**TCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA**T**GTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGT**CAG**CATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA**T**GGGGCTTTACGAAGCAGAATGGAGGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGT**CATT**GACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCATTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCCTCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA**GGA**ACTTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTA**AAAG**CCCAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA

**FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYF  
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNWF  
SACFDNFTEALAE TACRQM GYSRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSL  
HCLACGKSLKT PRVVG GEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV  
FNWKVRAGSDKLG SFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD  
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE  
GGVDTCQGD SGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGAGGAAACGCAGCGGCATCCCCAGGCTCCAG  
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC  
TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGCCGCGGGGGAGGCGGGCAGGGGCCCATGCCCC  
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  
CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGG  
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTA  
AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTACCCATCTCTACA  
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG  
AGGACAAGGTGATGGAGGGAAAAGGCCAAAGCCCCCTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG  
GGATGCTCTATTCTGGTACTATGAACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC  
CTGTCTCAAGACCGACAACCTCCTCCGTGGCTGCATCATGACGCTCCTTTGTGGCAGCCATCCCTTCGACCC  
AGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  
CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGG  
TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCAATCCGCCACGCGGTCTGTCTCCCGCCGATTCTCCA  
CAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT  
TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA  
CTTATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCT  
TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAATCTGGCGTGGAGTATA  
CACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCACCACAG  
GGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACC  
CTGAACCTGTTTCGAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGA  
GGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCTGGCGGGACCCCCACTGTGCCT  
GGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG  
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCCGAAATCATTA  
AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT  
GGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG  
ATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG  
ACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  
CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCT  
TTGCCTTAGTGCTTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG  
TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTAAAGCAGAGAGCAACACCTCCAGTCTCCAAGG  
AATGCAGGACCTCTGCCAGTGATGTGGACGTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  
CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG  
CAGCACAAAAGACCACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC  
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  
CAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAACATC  
TAAACAATCATATGCTAACATGCCACTCCTGGAAAACCTCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT  
TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC  
TTTCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAAATGG  
CAGGGGTAACTCTGAGCCTTCTTCACTCCTTTACCTTAGCTGACCCCTTACCTCTCCCCCTCCCTTTTCTTTGT  
TTTGGGATTGAGAAAACCTGCTTGTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAAAA

**FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ  
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA  
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAIPSTQVVYFFFE  
ETASEFDDFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFLLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN  
CSVYESCVDCLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP  
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
HFVTVTVLFLVLVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
SASDVDADNNCLGTEVA

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGGCTTCGGTAGAAG  
TGAGC**ATGG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGTCTC  
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
CCGGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
GTCCTTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG  
TGGCAGAGGAAAAATTTGAAAACCTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA  
GTTGAAACTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
CATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT  
CAGTATTCCGTTTCTTGTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG  
ATGTTCTTTAGTTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
GGAACATTTACAGAAGGCTCTAGGCCAGTTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
GGTTCATTAACCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC  
CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA  
ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
AAGTGTCAGTGTTCTCATTGGCCCAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA  
CTGGCTTCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG  
GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTTGGTGTCTTATTAGTT  
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
ACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC  
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
GGGGCCAGAAAGGTGAAGGAGAC**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC  
TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
TAATTTTGGCTACAAATTATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT  
CTTGTCTCCTTTGTTTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
GACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCTTCTCATGCGCCTCTCCGAA  
TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTTCTTTAGTTTCTGTTT  
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGC  
CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT  
TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTTCCAGATTTCTGAAAAATAAAAGTTTACA  
GCGTTATCTCTCCCCAACCTCACTAA

**FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPF  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV  
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF  
INSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLfvTHGGQ  
NSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPWHEQYLFDFVFVLLGLT  
LGT LWLCGKLLGMAVWVLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATAACCATGTT  
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGGCTACCCTGAAGCTCT  
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCCA  
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACCTGCAGTGACAGCAGGAGTAAGAGT  
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGC  
AGACTATCAGGGGTGCCGGCGGTGAGAAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGGCAG  
AGACCGGGGCACCTTGTGGGTTGCAGAGCCCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC  
TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
GGGTGGGCCCAGGAGGGGTTCAGAGCCCGTCCCTGCTGGAGGGGGAGTGCTGGTGGTCTGTGA  
GCCTGGCCGAGCTGCTGCAGGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCCCTGGGC  
GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGTC  
ACCAGTGGGGCCATCTACTTCGACCAGGTCCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
CTCTGGCTCCTTCGTAGCCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAG  
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC  
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA  
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT  
CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAAGGCCCAAGTCTTTCAAGCACAGAAT  
CCAGCCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCCAAGTTTAA  
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCACCCACCCACCCCAAGTTTACC  
CTCCACGCCACCTGCTGCATCTGTTTCCCTGCCTGTCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
AGAAGGAAGATCTGCACACTTTGCGGCCCTGTCTCCTCCGGTTCCTCCCAACCCCAAGCTTCTCT  
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCACG  
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC  
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCA  
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
GGCTGTCCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
GGTGAGTGTGTTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
ACCATGGAACCATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC  
CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCCTCCAGCTCTC  
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTTCTCCTGAT  
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCCTATTACCTGGGATTCCATGATTCATTCCTT  
CAGACCCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTTCTTATCCCGCTGTCCCATT  
GGCCCAGCCTGGATGAATCTATCAATAAAACAACCTAGAGAATGGTGGTCAGTGAGACACTAT  
AGAATTACTAAGGAGAAGATGCCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA  
TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAAATTAAAAA

**FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECLVVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32

164/249



## FIGURE 163

[illegible]

**FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGGRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLR EYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSM  
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK  
HKTKFGLPETEVLEVN

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-  
245, 318-323, 378-383

## FIGURE 165

GGGCGCGGGGATGGGGGGCGGGGGCGGGCGCCGCACTCGCTGAGGCCCGCCGACGAGGCCGGGGCGGGCGGGGCCA  
GGGCCGAGGAGCGCGGGCGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGGACGCCCGCGCGACGAGCAGGTGGCG  
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGGA  
CGGCTGTCTCTCAGCGAGGGGGCCGTGCACCCGCTCCTGAGCAGCGCCATGGCCCTGCTGGCCCTTCTGAAGACCCA  
GTTCTGTGCTGCACCTGCTGGTTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC  
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCCTCAACTGCCGCCTCGCCTACTCACTCTGGAGCCA  
ACTGGTCATGCTGCTGGAGTGGTGGTCTGTCACGGAGTGACACTGTTACACGGACCAGGCCACGGTAGAGCGCTT  
TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA  
GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAC  
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTCGAAGGGCTGAG  
GCGCTTGTGCGACTACCCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA  
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG  
CTTCACCACCGCAGTCAAGTGCCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCCTGAACCTCAGAGGAAA  
CAAGAACCCGTCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCTCT  
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA  
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCCTCCTGAA  
CTTCCTGTCTTGGGCCACCATTCTCCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTCTTTGCCAGCGGATCACC  
TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT  
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT  
CAGTCTCAAAAAAAAAAAAAAAAAACAAAAAACCCAGAAATTCGGAGTTGAACTGTGTAGTTACTGACATGAAAA  
ATTCACTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT  
TTTCAGGCTAATGAAAAAGAATGAAGGAAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA  
CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGGTCAGAAAGAAATGGCCACAAGCTGATGAAAAACA  
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA  
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG  
ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA  
AACCCTCAACTGTAATTATTGGACTTTTGGAGTCTTAGATGGTCCGTGACCTCTTTGTCTTCAGGGACAGTTTTTCA  
ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC  
TTACACCTGTAATCCCAGCACCTTTGGGAGGCCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT  
GAGTTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA  
ATTTCTTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCCTGTGATCCCAAGTAGCTTGGATTGTA  
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT  
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA  
GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGGAAATGTCTGTTCAAGTCCTTTG  
CCTTTTTAAATTTTTATTATTTATTTATTTATTTATTTTGTAGACAGGGTCTTGTCTGTTGCCAGGGCTGGAGTA  
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT  
AGCTGTATTTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA  
TGCCCAGGCTGGTCTTGAACCTCCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA  
CATGAGCCACTGCACCTGGCAAACCTCCCAAATTAACACACACACACAAAAAACACCTGATTCAAATGGGCA  
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG  
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

**FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLAYSLWSQLV  
MLLEWWSCTECTLFQDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK  
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN  
FLSWATILLSPLFSFVLGVFASGSPLLILTFVLGFVGAASFGVRRRLIGESLEPGRWRLQ

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

**FIGURE 167**

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTCTGCTTCCTG**TAA**TGTGGTATGCCATGGGGTCTTTCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTTAATGCTCTCATAAGACCACTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCACTAGGCCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

**FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR  
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

170/249

## FIGURE 169

GGCTGGGACTGGAAGTACCTGCTGCCCAAGTGATGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAAATCTGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
ACCGTCCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTA  
GCTGCGGCTTTC AAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT  
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGGACGGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT  
CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC  
ATCGAGTCTCCTGCATT CAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGGCTAATG  
GCTCAGTGTGTTGGCCCAGGAGGT CAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCC CAGGAGACTTTGATTTGAATTTGAAACCCCAA  
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

**FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA  
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

172/249



**FIGURE 171**

GC GGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCCTCCTGCCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT  
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCCGCGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
GCCCCGGAGCTGGGACGGCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC  
GGCTGAAGCCCGCCTTGAGACCCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTCAGGGTCTACATCAGCCTCCTGCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
**CTAG**GGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282  
><subunit 1 of 1, 262 aa, 1 stop  
><MW: 28809, pI: 8.80, NX(S/T): 1  
MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS  
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL  
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRRLKPALETLDELLAAGEAGTFDVAVVDA  
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS  
LLPLGDGLTLAFKI

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

[illegible]

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPKNKYPIFFFFGTHETAFLGPKDLFPYD  
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDRG  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSSSDSDSVVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEEREAKKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAQKPVKVERTRKRSEGFSDMRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAAEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDEKEHE  
EGRDSEEGPRCGSSDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

GTCTGGTTCTCCTGGATCTTACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATAATTA  
ACACCACTTTGAAAGAGAACATTGTTTTTCATC**ATGA**ATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
TTTTACACTTTTTCTGCTTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA  
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTCATC  
AGAAGGACTGGAATTTCAAACCTCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT  
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA  
ATTATGTAAATTAGCTGGGAAGATGCCAATACAGAATTGCTAAATTTTCATCAGAGTCTTGAGCCCTATAACAA  
AACTCACATATATGTGTGTGGAACTGGAGCAITTCATCCAATATGTGGGTATATTGATCTTTGGAGTCTACAAGGA  
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGACGC  
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTTGGCAAAGATACTGCAT  
CACTCGATCCCTTGGGCCCTACTCATGACCACCACCTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG  
AGCAAAATTTATTGGAACCTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG  
TGAATCATCTCAAGAAGGCAGTACCCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT  
AGGAGGACAACCGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAG  
TGATGGGGCAGATACCTTACTTTTGTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT  
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT  
CAGAGCAGTTTTTAAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT  
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCCACTGATTAAGTCCACCCGAGATTTTCCAGA  
TGATGTCAATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGATATACCCAGTTGCAGGAGGACCAACGTT  
CAAGAGAATCAATGTGGATTGATACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAGAAGATGGCCAGTACGA  
TGTAATGTTTTCTTGGAAACAGACATTTGGAACCTGCTCAAAGTTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA  
AGAGGTAGTGTGGAGGAGTTGCAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAAGCA  
GCAACAATTTGTACATTTGGTTCCCAGATGGATTAGTTAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC  
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC  
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAATAATGGCGACCCCAATCACCAGTGTCTGGACATCGAAGACAG  
CATTTAGTCATGAAACTGCTGATGAAAAGTGTATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATTGTATAC  
TAAATCCCCAACAGAACAATTAATAATGGTATATCCAGAGGTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCCGA  
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAAGGATTTCTGGGATGTATTTACTG  
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTATTGAGAATGAACAGATGGA  
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA  
CTACATCCAAATCCTTAGCAGCCCAAACCTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGGAGAAGCG  
GAGACAGAGAACAAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCAG**CTAG**TTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC  
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTTGCTAAGG  
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACCAGTTTT  
CCAAGAACAATCTTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTTACAGTTGTAATGTTTTTA  
TGTTTTGAGTTTTTGAATTTTATTGTCTATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT  
GCTTTTATTCCTCGAATGCTCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT  
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATATC  
AACAGGAACCTTTCTCAGTGAGCCATTTACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC  
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCT  
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA  
GCTCTACAGGGACAGAATGCTTAATAAATACCTTTAATAAGATATGGGAAAATATTTTAATAAAAACAAGGAAAACA  
TAATGATGTATAATGCATCTTATGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAGACAGCCAT  
AAATCTTGCTTTTGGGGAACTCATATCCCCATGAAAGGAAGAACAATCACAATAAAGGTGAGAGTAATGTAA  
TGGAGCTCTTTTCTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA  
AACTGCTAGCAAAATCTGAGGAAACATAAATTTCTTCTGAAGAATCATAGGAAGAGTAGACATTTTTATTTATAACC  
AATGATATTTTCACTATATATTTTTCTCTCTTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC  
CTTTATTTCTCTCCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA  
GAATTAAGAAAATGACATTTCTGGGGAGTGGGAGATATATATTTGTTGAATAACAGAACGAGTGTAAATTTTTAAC  
AACGGAAGGGTTAAATTAACCTCTTTGACATCTTCACTCAACCTTTTTCTCATTTGCTGAGTTAATCTGTTGTAAT  
GTAGTATGTTTTTTGTAATTTAACAATAAATAAGCCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL  
 GSSEGLDFQTL LLD EERGRLL LGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD  
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNGAKFIGTFF  
 IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC  
 SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP  
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPV  
 AGGPTEFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE  
 LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTY GKACADCC LARDPYCAWDGNA  
 CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA  
 TIKWYIQRS GDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLTLN  
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
 KGGPKWKHMQEMKKKRNRHRDLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

CCCTGACCTCCCTGAGCCAACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACC CGGGGAGCAGCA  
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCCACCAC  
CTCAGCACTTTCAGCCAGCAGGGAAGCTGATCAGGTGTGTGTCTGAGAGTGGGGAGCAGAAAGCGTGGCTGGCAAGA  
GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATTGGGCATC  
GGGTGAGGTGGGGGGGCACAGGTGTCTGTTGACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
AGCCATTGAGGTTGTCTGAGCTACAGAGGGGAGGGAAGGTATTTTAAAGTTAACAGTGTGGGCACAAATAGTTAA  
GAGCAAGTTTTTTGGAGCTAGACCAGACATAGGTTCAAATTTCTCTTCTGTTGCTTCCTAGTTTCTGTAGCCCCAGGT  
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
AGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAAAGTACCAGTCCCATAGTAAGTCTATGCCCCACAG  
TATTTCCACCCACCCCTGTCTCTGCTTCCCAACCAGGTAAGTCAACGAGCTGGAGCAGAGGGCGGCAGCAGGCT  
CAGAGCGGGAGGCTCCAGCATAGAACAGAGGTTACAGGAAGTGGCAGAGAGCATCCGCGGGCACAGGTGAGCG  
AGGTGAAGGGGGCTGCCCGTGGCCCTGCTGACGGGGCTGGCTTAGATGTGGAGCGTGGCTGAAGCCAGCCA  
TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC  
CCCAAGCCCTGGCCACGAGGGGCCCTCCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGGCAGGGCGTGAGGATG  
AGCTGACAATACCGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAGCAGCGCGAGGTAGGCTTTGCTCCCTGAGCGATATCTCAACTCCCAGGACCTCTCCCTCCGAGAGCAGCC  
AAGACAGTGACAATCCCTCGGGGGCAGAGCCGACAGCATCTCTGGCAGAGGCCCTGTACAGCTACACCGGCACAGA  
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGGCCCAAGATGGAGTAGATGACG  
GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTTGGGGTCTTCCCCTCCCCTGCTGGTGGAAGAGCTGCTTGGCCCC  
CAGGGCCACCTGAACCTCTCTGACCTGAACAGATGCTGCCGTCCCCTTCTCCTCCCAGCTTCTCCCACCTGCAC  
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG  
ACATGATGGCACCTCGACTCAGGCCGATCGCTCCACCACCTCCCCCGCCGCTAAAGCCCCGGATCTCGGCCACC  
CAGATCCCTCACCTGTAAGGCCAGGGAAGCCTTGACCCCTCAGTGATGCTGCTGCTCCCTATCTTCAAGCTGTCA  
CAGATCCCTCAATGATCCAGAGCAACACAGCCAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCCAAGGCT  
GGAAACTTGCCCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTTCCCATTTGTTCTATCATCTCTAGGAC  
GGAACCTACTACCTTCTCTTCTGTCTGATGACCTATCTAGGGTGGTGAAATGCCTGAAATCTCTGGGGCTGGAAACC  
ATCCATCAAGGTCTCTAGTAGTTCTGGGCCACCTCTTTCCCCACCTTGGCTCCATGACCCACCCCACTCTGGATG  
CCAGGGTCACTGGGTTGGGCTGGGGAGGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCAGCAAGGCCAGGCCAGGGCCTGGGCTCTTGTG  
CTAAGAGGGCAGGGGGCCTACGGTGCTATTGCTTTAGGGGCCACCACGGGCAGGGGGCTGCTCCCAGCTGCCAC  
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC  
TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCCT  
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCACCCCAACCCCTGGCCCTGCCAGCTGGTAG  
TCCATCAGCACATAGAAGGAGACTTGAGAAAGAGGAAGAATAACACTGTTGCTTCCCTGTTCAAGCTGTGTCCAGC  
TTTTCCCCTGGGGCTCCAGGACCTTCCCTAGCTCCACCCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGG  
AGTTTACTCTGGGGGTTTCAAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG  
TCAACAATGAGAGACCAGGAGTAGGTCCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCGACCCAGTGC  
AGTCCC GGCTGTGTTTTCTACCTGGTGATCAGAAGTGCTGTTGGTTGCTTGGCTGCCCATTTGCCCTCTTGTAGTGG  
CGAGCCCTGGGCTTGGGCCCCCTCCCTCGGGCCCTCAGTGTGGCTGCTGCAGAAGCTCTGGGGTCCCTTCAAGTG  
CACAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC  
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG  
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT  
TCTCAATGTGTGTACCCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG  
GCCCTCCCCTCTGACCAGGGACATCTGAGTTTGGTGGCTACTTCCCCTTGGCCTTAAAGTAGGGGAGGCCCTTCTC  
AGATTGTGGGGCAGATTGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAAGGCCACTT  
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA  
CAGAGAACACAGTGGTCTCCCCTGTCCGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG  
GCCTCTTGTGTCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC  
CGTCTGTCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT  
TCATGTTTTGTTTTCTACGTTCTTTTTCAGCATGCTCCTTAAACCCAGAGCCCCAATTTCCCCAAGCCCCATTT  
TTTTCTGTCTTTATCTAATAAACTCAATATTAAG

**FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEPPAPQALATRALPCPAHVVFQYQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGVFPERYLNFPDLSLPSSQSDNPGAEPTAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPPELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT



CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGACAGAGTCTTACAGAGGGAGAGGCCAGAGAAGCTGCAGA  
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG  
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTTCTCCATTTCTTTAACGGTCTCTCAGCCCTCTGAAAAACTTTGCC  
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTTGGAGGACTTTGGT  
GCCCTAGACGGCTCAGTCCCTCCCAGTGCAGTACCAGTGCCATGCCCCAGACAGGCTCGCATCCCGGGAGGGG  
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTTGCTCTCTGCTCCCCATTGTGCCGCTCTCTGGCTGGTGTG  
GCTGCTTCTGCTACTGCTGGCTCTCTCTGCTGCTCAGCCCCGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT  
CGTGTCTTCCAGAGAAGCTCAACGGCAGCGTCTTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA  
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGCAGGGGCTGACAGTGCAGTA  
CCTGGGCCAGGCGCTGAGTCTGCTGGGTGGAGCAGAGCTTGGCACCCTACCTGACTGGCACCATCAATGGAGATCC  
CGAGTCGGTGGCATCTCTGCACTGGATGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGCTGAACTCCA  
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCTACGCCGGAAGAGTCC  
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCCGAAGAGCCAA  
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC  
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCACCCAAGCATCCGCAATCG  
TGTGAGTCTGGTGGTGACTCGGCTAGTGATCCTGGGTGAGGCGAGGAGGCTCCCAAGTGGGGCCGAGTGCTGC  
CCAGACCTTCGCGAGTCTCTGTGCTTGGCAGCGGGGCTCAACACACCCCTGAGGACTCGGGCCCTGACCACCTTTGA  
CACAGCCATTCTGTTTACCCGTGAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGG  
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA  
TGAATCGGCTCATGTCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCCTTTGAGCAC  
CTCTCGCCATGTCAATGGCCCTGTGATGGCTCATGTGGATCTTGAGGAGCCCTGGTCCCCCTGCACTGCCGCTT  
CATCACTGACTTCTCTGGACAAATGGCTATGGGCACCTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT  
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCGACTCACGCCATTGTCC  
ACAGCTGCCCGCCGCTGTGCTGCCCTCTGGTGTCTTGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA  
CTCGCCCTGGGCCGATGGCACACCTTGCGGGCCCGCACAGGCCCTGCATGGGTGGTGGCTGCCTCCACATGGACCA  
GCTCCAGGACTTCAATATTTCCACAGGCTGGTGGCTGGGTCTTGGGGACCATGGGGTGACTGCTCTCGGACCTG  
TGGGGTGTTGGTTCAGTTCTCTCTCCCGAGACTGCACGAGGCTGTCCCCGGAATGGTGGCAAGTACTGTAGGG  
CGCGCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
GTGTGCTGCCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCCAGGGCCCATGGACTGGGTTCCTCGCTACAC  
AGGCGTGGCCCCCAGGACCAGTGCAAACCTACCTGCCAGGCCCCGGGCACCTGGGCTACTACTATGTGCTGGAGCC  
ACGGGTGGTAGATGGGACCCCCCTGTTCCCCGGACAGCTCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG  
CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTCACTGTGTGCGGAGGGGACGGTTCTGGTTGACG  
CAAGCAGTCAGGTCCTTTCAGGAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA  
CATTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA  
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTA  
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTACGGCCATGGGCCACTGGCCCAGCCCTTTGACACTGCAAGTCCT  
AGTGGCTGGCAACCCCCAGGACACACGCCCTCCGATACAGCTTCTCTGTCGCCCGGCCACCCCTTCAACGCCACG  
CCCCACTCCCCAGGACTGGTCTGACCAGGAAGACACAGATTCTTGAGATGCTTCCGGCGCGCCCCCTGGCGGGCAG  
GAAATTAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT  
CTGTTGCTGCCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCTCTCTGCCCTAAT  
GCGCAGGCTGGCCCTGCCCTGGTTTCTTGCCCTGGGAGGCAGTGATGGGTAGTGGATGGAAGGGGCTGACAGAC  
AGCCCTCCATCTAAACTGCCCTCTGCCCTGCGGGTACAGGAGGGAGGGGGAAGGCAGGGGAGGGCTGGGCC  
CAGTTGATATTTATTTAGTATTTATTTATTTATTTATTTAGCACAGGGAAGGGGACAGGACTAGGTCCTGGGAA  
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG  
TGTGTATGCGTGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTCT  
TTCTGAATTTTATTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCTTCAGGGAGTGAGGGATTATCTTTT  
TTTTTTTTTCTTTCTTTCTTTCTTTTCTTTTCTTTTGGAGACAGAATCTCGCTCTGTGCGCCAGGCTGGAGTGCAATG  
GCACAATCTCGGCTCACTGCATCTCCGCCCTCCCGGTTCAAGTGATTTCTCATGCCCTCAGCCTCCTGAGTAGTG  
GGATTACAGGCTCCTGACCACACGCCAGCTAACTTTTGTTTTGTTTGTTTGGAGACAGAGTCTCGCTATTGTC  
ACAGGGGCTGGAATGATTTTCAAGCTCACTGCAACTTTTCCGCCACCTGGGTTCCAGCAATTTCTCCTGCCCTCAGCCTCC  
CGAGTAGCTGAGATTTATAGGCACCTACCACACGCCCGGCTAATTTTTTGTATTTTATAGTAGAGACGGGGTTTAC  
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCCTTCACTCCCCAAAGTGCTGGGATT  
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCACTAATTTTGTGATTTTATAGTAGAGACAGGGTTTACCATTGT  
TGGCCAGGCTGCTCTTGAATCTGCTGACCTCAGTAACTCGACCTGCCCTGCCCTCCCCAAAGTGCTGGGATTACAGT  
TGTGAGCCACCAAGCGCCGGTACATATTTTTTAAATTTGAATTTCTACTAATTTATGTGATCCTTTTGGAGTCAGACG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAGGAAA

**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV  
 FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP  
 GTYLTGTINGDPESVASLHWDGGALLGVLQYRGAEHLQPLEGGTPNSAGGPGAHLRRKSP  
 ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA  
 AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF  
 DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD  
 NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
 PVTFPKGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG  
 PAQACMGGRCCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVRNGGKY  
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK  
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG  
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL  
 MPSPTDVVLPGAVSLRYSGATAASETL SGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
 PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
 582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATG**G  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT  
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
TTAAAGTGATTTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY  
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT  
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKN SKILEICDNVTMYWI  
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY  
TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV  
ARMLGRV

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA  
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
GGCACCCCTGCTTTGCCTGTCTTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGA**GTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGAAGTGGGAGTTTGGTCAGTGGGGT  
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

### FIGURE 185

GAGCTCCCCCTCAGGAGCGGTTAGCTTTCACACACCTTCGGCAGCAGGAGGCGGCAGCTTCTCG  
CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCT  
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
GCATGGGTGGGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTCTG  
GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG  
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
ATATACGATGGAGGTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA  
AACAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA  
TTTCCCAGCTTATCCCCAAGAAAACCTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
CTGCTGTTTGAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACTTACTGAAGAA  
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
TGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG  
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG  
TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA  
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT  
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
GCATACACCTGTAGTCCCAGCATTCGCGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
TCCTGTCTAAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA  
ACTAATTCTTTAA



**FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

### FIGURE 187

GGAAAAAAGCTGTTCTCTTCTGTGGCAGAGAACCTTGCTTCAAAGCAGAAAGTAGCAGTTCCTCG  
GAGTCCAGCTGGCTAAAAGCTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG  
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACCTTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC  
TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTGGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGGT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC  
CATGCAATGACAAAATCTATATTACTTTCTCAAATGGACCCCAAGAACTTTGATTTA  
CTGTTCTTAACTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTCAAGCAGAAATGAGATATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA  
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAGGAAATTGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT  
TTCTTGTGTATTAAATTAACATTTTTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGTTTAGTTTTACTAAA  
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA  
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA  
TTAATAAATTGTACATTTTTTCTAATT

**FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTCATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGTTGCTGTGCTGCACTT  
GCCCCTCGGGGGGTCCAGGGCCCCAGCCATTACATGGCCCCGCTACTCAACATCTGCCCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTC**TGA**CGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT  
CGTACCTTTTGTTTCTGCCTCCTGCTATTTTTCTTTGACTGAGGATATTTAAAATTCATTT  
GAAAAGTGAAGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCCACCTCCGGAACCTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTTACACTCACATTTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

**FIGURE 190**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM  
QCKVYDSLLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP  
SGGSQGPPSHYMARYSTSAPAISRGPPSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

193/249

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC  
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
TGGGAAGGGCTCTGG**ATGA**ATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACTTCAGGAGTCCTCTTCATCCTGAC  
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCT**TAA**TGCCTCCTTTTGGCTCCAAGT  
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

**FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV

**Important features of the protein:****Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

195/249

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATG**AAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAAACACGTCAATAAAAAAATAATCTCCCAGA



**FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN  
ECHLCTESLKSNGRVQFLHDGSC

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCC**ATG**GCTGCCTCCCCCGCGCGGCCTGCTGTCTTGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCTTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTC  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

**FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTTKKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDIYQRHYD  
EDSAIGPRSPYGFRRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

199/249

**FIGURE 197**

CGGCTCGAGCCCCGCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCCCTGCCTTCTGGTGCTGGCCCTTGCCCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTGAGGGACCCCAACGCCATCCCAGCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTCACAGCAACACCGCCAG  
CCCCGGA CTCCCCGCAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG  
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCTGCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC  
GGACCTTGCTCCCCGCGCCGCGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA  
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA  
AAAAAAA

## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPPNPCCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

## FIGURE 199

[illegible]

**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHCAKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

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**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
 CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
 AATTTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACACGC  
 TTGGGGTGAACTTGGGTCCTGTGGTTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACACGC  
 TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAAGTTGAACATGAC  
 CTGTTGCATTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT  
 TGCACCCTCCCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGAGCCTGGACCCAC  
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCCGAGGTGCGG  
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
 CCAGGGCCTTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
 GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTCGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT  
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTGCGACATTCCACTGG  
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT  
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGAGATTCACTTTGGCAGCCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC  
 AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGCGGATTTGACCA  
 GATAAATGCTGTGGATGAACGA**TGA**ATGTCAATGTCAGAAGGAAAAGAGAATTTTGGCCATC  
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA



**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR  
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVS  
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGGSVEILPCSRVGHIYQNQDSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLGCRTFHWFLANVYPEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEEGLAIHQHWDFQENGMIVHILSGKCM EAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGAC**ATGGA**  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCCCTCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCCTGCCTGGCACTG  
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTTGAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCTGCGGCCATT  
 CTGTTCCGGGGGCCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCCACCC  
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
 CTCCACAGCCCCTGGCCCTCCCAAGGGGGCTGGACAGCTCCTCTCTGGGAGGCACCCCTTC  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTCTGCCC  
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACTCTGCCCTCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCCCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCAATGTTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGGCCGCACAGCCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTGCACACCACCCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGCACTACCTCCACCTTCAC  
 AGGCCATTTGCACACGCTCCTGCACCCCTCTCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGG  
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCTATGG  
 TCTCGTCCCATTTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGGCCAGACTTCACCCCCAGCCCA  
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG  
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT  
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGACTCCCTCCTGTCCCCCTCCTTT  
 CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTGCTTCCCTGCCCTTCCCCCTCCTCAGGTT  
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTTCCCTTCTTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATTATCTCTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAAATTTTCAAATAAAGCCTTTGCAAGATAA

## FIGURE 204

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
```

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIITYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATGG**  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCTGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA  
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

**FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG  
PPAPTVPAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC  
CCAGAGGCGCTGGGAGTGTGGCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG  
ACTCGCACGTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC  
CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGT  
CCCACAGGTCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC  
TGGCACAAGTAAGTCCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

**FIGURE 209**

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCCGTCCAGGTTTCATGTTCCCTCTTATTTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTATTCAACAGCG  
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAACATAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCT**TGA**CTTCTCCTTGGAACATACATATGGCC  
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG  
 GATCACTAGGCCTGCCAACCACACACACACGACGACGTGCACACACGACGACGCGTGCACAC  
 ACACACGCGCACACACACACACACAGAGCTTCATTTCCCTGTCTTAAAATCTCGTTTTCTC  
 TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCC  
 TATGTAAATCAACAACCTGCATAATAATAAAAAGGCAATCATGTTATA



**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSFQISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQKGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

213/249

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGAGGTGCCACCCGGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGGAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG  
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTCCACTACTC  
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCTTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC  
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA  
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC  
AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
AAATGTGTCATATCAATTTCTGGATTCAATAGCAAGATTAGCAAAGGATAAATGCCGAAG  
GTCACCTTCACTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT  
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

**FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

215/249

**FIGURE 213**

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGA CTGCCCGGGCTGCCGCC  
CCCGGGGGCTTGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGGCTGCCGCC  
TCTCGGCCACGGCTGGGTGCGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCTGAGGCG  
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT  
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA  
TATGAAGGTGAAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCTG  
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT  
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA  
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTC AATTGAAT  
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAAACA  
TGTTTATAAAGTAAAAAAA

**FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTROLLSHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT  
GGTGC GCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCGTCCTGTTTCCTCATGATGTCAGG  
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG  
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG  
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLLMAVAAPSRRGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRIPRRPGALDGLEA  
GGYVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGGSGLCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCTCCGGGGGCCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC  
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAACTCTACCAGCATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTTGCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT  
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC  
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
 CTGGACACCTGTGCTGGACCCACACGGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
 CCCATGCACCTGCTGTCCCTTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAGCATTTGCTCTG  
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCCTGAGCTG**TAA**CCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT  
 GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA  
 ATAAACACTTTTAAATGATCAAAAAAAAAAAAA



**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFSPMSFLRRKVIPET  
EQAGVLNWFRVPLHSLACLGLLVLHDSRKTGTRNMF SICSAVMMALLAVVGLFTTVVRHDA  
ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**  
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
CGGCTTCCGTATCCATGATTATTTGTA**CTT**CAAGTGCTGAGTCCTGGGGACATTCGATACA  
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
TGG**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
AGGAATTTTGTACTTGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
AGTGGTTTAAAGAGCTGGTGT**TTT**GGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT  
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 222**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538  
><subunit 1 of 1, 116 aa, 1 stop  
><MW: 12910, pI: 6.41, NX(S/T): 1  
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW  
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCM DLSQRYCLMAVFNV IYLENEDSE

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTACAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

**FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK  
LGDSWDVKLGALGGNTQEVTLPGEYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISS  
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

GCTGAGCGTGTGCGCGGTTACGCGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
GAACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
TTTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATAT  
CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTTGCTGCGAATGCGGTGTTGGGATT  
TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG  
ACAGGGGCTGTCATGCAACTGGCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAA  
CAATACAAAGG**ATG**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAAGTTAAGTATAAT  
CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
TCTCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC  
TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGBAAGCTGCTGAGTTT  
ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
ATGATCAGACTCAAAGAAGTTTACCTGGAGCACAAATCAATTTTTCCAAGCTCAACCTGGCCCT  
TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTCTAG  
GACAGACCATGTCCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
GAAGCTTTTCAGTGGACCCAGTGTTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA  
TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTG  
AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT  
TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT  
GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGCGCGCTTTTCTGTCCG  
TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCTTGCAGCATGAAGCAG  
CTGCAGCAGCGTCCCTCATGCGAAGGCACAGGAAAAAGACAGTCCCTAAAGCAAAT  
GACTCCCGAGACCCAGGAATTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA  
TGCTGCTGAATGGGACGGGACCTTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC  
TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG  
CAAGATCCTTCCTTGTCCGTTTTAGTGCATTCATAAATACTGGTCAATTTTCCCTCTCATACATA  
ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGTCCGGTTTTAATATAA  
TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTCGCATTTGTTTTAAGATAAACT  
TCTTTCATAGGTAAAAA



**FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG  
 CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF  
 LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL  
 DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLQWNLKISVIGQTM  
 SWTWSSLQRLDLGNEIEAFSGPSVFQCVPNLQRLNLDLSDNKLTFIGQEILDSWISLNDISLA  
 GNIWECSRNICSLVNWLKSEFKGLRENTIICASPKELOQGVNVIDAVKNYSICGKSTTERFDLA  
 RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI  
 LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTTETSEMLLN  
 GTGPCTYNKSGSRECEV

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
TAAATATGTCAGATCCAGACTTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGTATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG  
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
AAACATCAATAGATATCTAAAAA

## FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
```

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT  
 CCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAA**ATG**TTTTTTA  
 CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTACTGTTGCTTGTATTTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGAT**TAG**CAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC  
 TCTAATCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG  
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCAATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA  
 AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAGTGTTAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAATAAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCACAGGGAACCCTAATCTTGGGTAAATCTAGTATAAAACAAATTATACTTTTAT  
 TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTCATAGTATTTATT  
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
 TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA  
 TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

**FIGURE 230**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL  
VPVTTNKRTNVSGSIR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGGCCGCCGGGGTGAAGCTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA  
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCCGGGCT  
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTACTGCC  
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG  
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
 CACAACCTCATTACCCGCCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCACCAT  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
 TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG  
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGACCTGTGCGGCAACCCCAAGCTTAACT  
 GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
 AACCTGGTGCCCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  
 ATCTTGT**TGA**CAAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCTCTGGGCTGCCTCAG  
 GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA  
 GCGTCACCACAGGAGTTGTGGGCCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCAAGTGCTTCCCTCAT  
 GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT  
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC  
 AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCCGACCCAATGCACTTTCTTGTCTCCTCTA  
 ATAAGCCCCACCCCTCCCCGCCTGGGCTCCCTTGCTGCCCTTGCTGCTTCCCCATTAGCACA  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC  
 CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGGCCTCCTGGATTCACTCCCCACTGGCCCTGAGCACGACAGC  
 CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCCGACCATGTCTATGC  
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCCTTAGTCTTCATTTTA  
 TAAAAGTTGTTGCCTTTTTTAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCAATTTGTAAAAGCAGAAAAAGGTGCAATTTGTTCACTTTTGTAAAT  
 ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC  
 CCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVSAFTTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS  
GFRELPGLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

## FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA  
AAACAAGTTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCA  
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC  
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC  
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC  
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT  
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT  
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT  
ATTTTTTTTACTTGACATGAACTTTAAAAAAATTACAGATTATATTTATAACCTGACTAG  
AGCAGGTGATGTATTTTTTATACAGTAAAAAATAAACCTTGTAATTCTAGAAGAGTGGCT  
AGGGGGGTTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTGCATA  
CCAAAAAAAAAAAAAAAAAAAAA



**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSTLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

237/249

CGGTATACGTCCTTGCGCTACTGCTGA**ATG**TCCGTCCTCCGAGGAGGAGGAGAGGAGGCTTTTGCCTGCTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCAGACGCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTTCAAGTGCAAATGGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGCGATTCGTGGTGTACATCATGCATTTGCCAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCCGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTT**TAA**

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH  
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTFWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAA**ATG**GCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTTCATGTTGATGTTTGGGTCACCTATTGCTTCCATGTGGATTCTTTTTTGGTGC  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA  
TATTTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGAC**CTG**AGATCAC  
TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTTATGTTT  
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTTATTCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAAGGTTTTAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA  
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTTAAATGCCC  
AAAGGACTAGTTTGAAAGCTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
CTGGCGGGCCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT  
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  
**GATG**AGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
TGTTTATTCTGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
GCCTCGCCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
AGCCAACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGGTGCACTGGTGTCTGGTGG  
CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG  
GGGAGTTCCTACGCAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG  
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTT**TAG**GGTGGC  
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCCG  
GCAGGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCTTGCACGC  
TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCCACAGCACATCCTACCCGGAAGACC  
AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTCGTCAGGG  
ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
TTTTTGCTGGTTTTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRLKFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCCTAGTCCTCTAGTCCTCAAATCCCAGTCCC  
 CTGCACCCCTTCCTGGGACACT**ATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC  
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA  
 GCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGAGC  
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTTCAGAAAGGATC  
 CCCAGGGGGGTTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
 CCTTCTCCTGGCTGTTTTATTTCAATTGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTTCACCTCAGCACAAAGCCACGACTGAGGCAT**TAA**ATTCCTTCTCAGATACCA  
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG  
 GAAGTTTGGGATATACCCCCAAAGTCCTCTACCCCCCTCACTTTTATGGCCCTTTCCTAGATA  
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA  
 TATTTGGAAATTAAAGTTTCTGACTTT



**FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPPASYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ  
INSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT  
L FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 243**

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC  
GTGGACCCAAAGGTAGCAATCTGAAAC**ATG**AGGAGTACGATTCTACTGTTTTGTCTTCTAGG  
ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC  
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG  
ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG  
AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC  
TGCACCCACATGTGTTACCAATTTTTGTACACAACCTTGAGCCCAGGGCACTATCCTAAGC  
TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCAT  
CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG  
GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCGCCTCCCAACTCCCAGTGGC  
ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA  
GGAAGCCACCACAGAATCAGCAAATGGAATTCAG**TAA**GCTGTTTCAAATTTTTTCAACTAAG  
CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA  
GACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATTTACCTGAAAATATTCTTGAAATT  
TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT  
CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAAAACATATTTGAAA  
ACTGGAAA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

GGAGAGAGGCGCGCGGGTGAAGGCGCATTTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG  
GCAGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG  
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG  
GAGTCCTGGACACCCAACCTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
AATGGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTCACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAATTACCCAAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**  
**A**ATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT  
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAAATA  
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT  
AAAAATTATTTCCAACA

**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSP  
EMNSTINIHRITSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRITIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

249/249